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Database
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Maximum DB seq length: 2000000000
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1853
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2: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT: *
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3: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1982.DAT: *
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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346	346	346	346	346	346	346	346	346	346	Length I	
23	23	23	23	23	23	22	22	22	22	H	
AAE17077	AAU11401	AAE16172	ABB08596	AA014788	AAE24354	AAG80968	AAU04373	AAU06197	ABB44522	ID	
Human G-protein co	HM74-like G-protei	Human G-protein co	Human lipocyte-ori	Human purinergic-1	_	Human nGPCR11 #2.		human	Human GPCRla polvo	Description	

4.5	44	43	42	41	40	39	Ж	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11
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ABB05229	AAG77965	AAE17231	AAU10004	ABG66684	9	AAU07294	AAU04383	AAU04368	AAE07538	AAB82852	AAE12022	AAE07539	AAG77964	AAM52651	AAY90659	AAY90625	AAE16376	AAY79157	AAW88461	AAY94339	AAU04365	AAG78785	AAW88460	AAU74911	AAE02493	AAU77993	AAU79041	AAY90637	AAY90672	7	AAW94654	799	8093	ABB44523 ·
LTD4-like	G-prote	Cysi		nove	LTC4 recept	inyl leukot	G-protein	G-protein	G-protein	P2Y-like G	n G-protein	G-protein	G-protein	G-protein	mutant G	G protein-	G-protein		7-tra	cell surfac	_	opioid-type	7-tra	acid seg	CON	inflamm	G prote		mutant G	a	rt	inflamma	nGPCR11 #1.	Human GPCR1c polyp

ALIGNMENTS

standard; Protein; 346 AA.	ABB44522 standard; Protein XX XX AC ABB44522; AC ABB44522; XX DT 28-JAN-2002 (first entry)
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Human; GCPR; G-coupled protein-receptor; cardiant; antiarteriosclerotic; anabolic; cytostatic; antiviral; gene therapy; cardiomyopathy; obesity; anorexia; diabetes; osteoporosis; Crohn's disease; multiple sclerosis; asthma; Alzheimer's disease; Parkinson's disorder; Huntington's disease; infection; human immunodeficiency virus; HIV.

Homo sapiens.

WO200174904-A2

11-OCT-2001.

30-MAR-2001; 2001WO-US10241.

31-MAR-2000; 05-APR-2000; 06-APR-2000; 06-APR-2000; 06-APR-2000; 06-APR-2000; 06-APR-2000; 06-APR-2000; 06-APR-2000; 2000US-194614P. 2000US-195063P. 2000US-195066P. 2000US-195067P. 2000US-195068P. 2000US-195069P. 2000US-195070P. 2000US-195070P. 2000US-193664P

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11-OCT-2000;
18-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                             sclerosis, asthma, cancers, neurodegenerative disorders (e.g. Alzheimer's disease, Parkinson's disorder, Huntington's disorders, immune disorders, haematopoietic disorders, developmental diseases, neurological disorders, bacterial, fungal, protozoal and viral infections (e.g. with human immunodeficiency virus (HIV)-1 or HIV-2). They can be used diagnostically to determine the presence of or predisposition to a disease associated with altered levels of the polypeptide in mammals (especially humans) by detecting alterations in polypeptide expression levels relative to control samples. They are useful to identify agents binding polypeptide (e.g. cellular receptors or downstream effectors) and/or agents modulating cellular polypeptide expression or activity, useful as antagonists and accomists in disease transmitter.
                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polypeptides can be administered therapeutically, especially using gene therapy and expressing the encoding DNA in vivo, to treat or prevent GPCRX associated disorders, especially in humans. For example, they can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 encode G-coupled protein-receptor related polypeptides (ABB44522-ABB44543). The isolated polypeptide having a sequence differed by no more than 15% of amino acid residues from one of 22 amino acid sequences (or mature forms of the sequences), fully defined in the specification and corresponding to human G-protein coupled receptor X (GPCRX) polypeptides. The polypeptides have potential cardiant, antiarteriosclerotic, anabolic, cytostatic and antiviral activity. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 8; 157pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New human G-protein coupled receptor X, GPCRX, polypeptide useful in treatment or prevention of GPCRX associated disorders e.g. cardiomyopathy or atherosclerosis, and to screen for antagonists and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 be used to treat/prevent cardiomyopathy, atherosclerosis, disorders related to signal processing and metabolic pathway modulation (e.g. obesity, anorexia), diabetes, osteoporosis, Crohn's disease, multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   agonists useful therapeutically
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Padigaru M,
                                                                                                                                                                                                                                                                                                                                                                                                                  antagonists and agonists in disease treatment.
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181 FQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240
                                           121
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                                                                HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM 180
                                                                                                                                                                                                                             MYNGSCCRIEGDTISQWMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA 60
                                           HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM
                                                                                                                            DFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120
                                                                                                                                                                   DFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120
                                                                                                                                                                                                            MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA 60
                                                                                                                                                                                                                                                                                            346;
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2000US-21184P.
2000US-221325P.
2000US-224588P.
2000US-229613P.
2001US-262508P.
2001US-263433P.
2001US-263434P.
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Mishnu VS,
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2001US-0823172
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Tchernev VT,
                                                                                                                                                                                                                                                                                            0,
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                                                                                                                                                                                                                                                                                              Mismatches
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Spytek KA,
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RESULT 2
AAU06197
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                                                                                                                                                                                                                                                                   Novel human G-protein coupled receptor proteins and nucleic acid molecules encoding the protein for use in developing human therapeutics and diagnostic compositions and for identifying modulators of the
                                                                                                                                                                                                                                                                                                              N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                     27-MAR-2000; 2000US-192419P
06-SEP-2000; 2000US-230459P
20-SEP-2000; 2000US-0666535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hyperproliterative disorder; neurological disorder; inflammatory disorder; respiratory disorder.
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                                                                                                                                                                                                                                     Claim 1;
                                                                                                                                                                                                                                                          protein
                                                                                                                                                                                                                                                                                                                                              Ye J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; G-protein coupled receptor; GPCR; chemokine receptor; protease; hyperproliferative disorder; neurological disorder; psychiatric diseas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel human G protein-coupled receptor (GPCR) protein.
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                                                                                                                                                                                                                                     Fig 1;
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                                                                                                                                                                                                                                                                                                                                                Beasley EM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       240
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psychiatric diseases (e.g. schizophrenia), inflammatory disorders (e.g. diabetes) and respiratory disorders (e.g. adult respiratory distress syndrome, ARDS). The GPCR protein is also useful for identifying a modulator of the expression of the protein. It also serves as a target for identifying agents for use in mammalian therapeutic applications, e.g. a human drug, particularly modulating a biological or pathological response in a cell or tissue that expresses the protein, in biological assays related to GPCRs that are related to members of the chemokine assays useful in diagnosing a disease or predisposition to assays. GPCR is also useful in diagnosing a disease or predisposition to a disease mediated by the peptide, in pharmacogenomic analysis. polynucleotide sequences can also be used in gene therapy. The persents the novel human GPCR of the invention. The present invention relates to the isolation of a novel human G-protein coupled receptor (GPCR) which is related to the chemokine receptor subfamily. The cDNA and gene sequences encoding for GPCR are also given in the invention. The sequences of the invention are useful for diagnosing and treating diseases or conditions mediated by human proteases. Such diseases include hyperproliferative disorders (e.g. hyperplasia), neurological disorders (e.g. Parkinson's disease),

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14 - WAR - 2000

10 - APR - 2000

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28 - APR - 2000

12 - WAY - 2000

12 - JUN - 2000

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21 - AUG - 2000

26 - SEP - 2000

26 - SEP - 2000

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20 - OCT - 2000
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23-DEC-1999;
11-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                             inverse agonist;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDPHIVEWH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DFILMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120
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2000US-0235418.
2000US-0235779.
2000US-0242332.
2000US-0242343.
                                           2000US-0210741.
2000US-0210982.
2000US-0226760.
                                                                            2000US-0189258
2000US-0189259
2000US-0195898
2000US-0195899
2000US-0196078
2000US-0200419
2000US-0203630
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                                                                                                                                                          99US-0171902.
2000US-0181749.
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                                                                                                                                                                                            99US-0171900
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                                                                                                                                                                                                                                                                                                                                                    coupled receptor; GPCR; hRUP19; agonist;
                                                                                                                                                                                                                                                                                                                                            lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
                                                                                                                                                                                                                                                                                                                                            cancer
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Pred. No. 1.5e-199;
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          6 protein-coupled receptor; nGPCR; seven transmembrane receptor; signal transduction; schizophrenia; thyroid disorder; renal failure; rheumatoid arthritis; CNS disorder; infection; metabolic disease; cardiovascular disease; proliferative disorder; hormonal disorder; neurological disorder; neuronal disorder; Alzheimer's disease; cancer; attention deficit hyperactivity disorder/attention deficit disorder;
Parkinson's disease; migraine; senile dementia; inflammatory
                                                                                                                                     Human nGPCR11 #2.
                                                                                                                                                                                                                                       AAG80968 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hRUP19. The endogenous and non-endogenous, constitutively activated versions of human G-protein coupled receptors (GPCR), are useful for direct identification of candidate compounds as receptor agonists, inverse agonists or partial agonists having applicability as therapeutic agents for treating diseases related to GPCR, e.g. lung cancer. Non-endogenous version of human GPCRs are also utilized in research settings and in vitro and in vivo system, incorporating GPCRs can be utilised to elucidate and understand the roles these receptors
                                                                                                                                                                      28-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Endogenous and non-endogenous versions of human G-protein coupled receptors for direct identification of candidate compounds as agonists, inverse agonists or partial agonists for use as therapeutic agents -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence represents a human G-protein coupled receptor (GPCR), hRUP19. The endogenous and non-endogenous, constitutively activate
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                                                                                                                                                                                                                                                                                                                   QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDPHIVEWH 346
                                                                                                                                                                                                                                                                                                                                                                                                       LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DFLLMICLPERTDYYLRRRHWAFGDIPCRVGLETLAMNRAGSIVELTVVAADRYFKVVHP 120
                                                                                                                                                                                                                                                                                                                                                                                     LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                   FQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLDSVSAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM
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)B; AAS07946.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the human condition, both normal and diseased.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Page 110-111; 160pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              346 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                       Protein; 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lowitz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 1853; DB 22; 100.0%; Pred. No. 1.5e-199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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Best Local :
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20-APR-2000;
02-MAY-2000;
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28-DEC-1999;
22-FEB-2000;
28-FEB-2000;
28-FEB-2000;
02-MAR-2000;
03-MAR-2000;
                                                                                                                                                                                                          treating neurological disorders, including schizophrenia, ADHD/ADD (attention deficit-hyperactivity disorder/attention deficit disorder), and neuronal disorders such as Alzheimer's disease, Parkinson's disease, migraine and senile dementia. Additional disorders include inflammatory conditions (e.g. Crohn's disease), rheumatoid arthritis, autoimmune disorders, cancers, respiratory ailments such as asthma, and inflammator
                                                                                                                                                                                                                                                                                                                                                           nGPCRx coding sequences are useful for screening a human to diagnose a disorder affecting the brain or a genetic predisposition, specifically schizophrenia. nGPCRx are useful for identifying compounds useful for treating schizophrenia. Detection of nGPCRx in a sample is useful as a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAH51008
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17-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rheumatoid arthritis; autoimmune disorder; respiratory ailment;
                                                                                                                                                                                                                                                                                              diagnostic tool for diseases or disorders e.g. thyroid disorders, renal failure, rheumatoid arthritis, CNS disorders, infections such as HIV-1, metabolic and cardiovascular diseases, proliferative disorders and hormonal disorders. Modulators of nGPCRx activity have the utility for the disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                          sequence is one such G protein-coupled receptor. GPCRs are also known as seven transmembrane receptors and function in signal transduction. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to novel G protein-coupled receptors (nGPCRx; where x is 1, 3, 4, 5, 9, 11, 12, 14-18, 20, 21, 22, 24, 27, 28, 31-38, 40, 41, 53-60) and their coding sequences. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 37; Page 89; 261pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New G protein-coupled polynucleotide useful
                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (PHAA ) PHARMACIA & UPJOHN CO.
                                                                                                                                                                                         diseases e.g. inflammatory bowel disease
        61
                                                                                                                Local Similarity
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      DFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120
                                                       MYNGSCCRIEGDTISQYMPPLLIVAFVLGALGNGVALCGFCEHMKTWKPSTVYLFNLAVA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001-389826/41.
                                       MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA
                                                                                                   346;
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2000US-0185421
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2000US-0186530.
2000US-0186811.
2000US-0190310.
2000US-0190310.
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2000US-0201190.
2000US-0203111.
2000US-0203111.
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                                                                                                              100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      receptor (nGPCR-x) for diagnosing and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              di LA, Hiebsch RR, Li
Bannigan CM, Ruff V,
                                                                                                   0;
                                                                                                                Score 1853; DB 22;
Pred. No. 1.5e-199;
                                                                                                     Mismatches
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V, Sejlitz T, Hui
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      e.g. schizophrenia
                                                                                                     Indels
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RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   adipocyte;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       autoimmune disorder; psoriasis; multiple sclerosis; brain disorder; degenerative disease; Alzheimer's disease; Pick disease; diabetes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FQLEFEMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              anorectic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hyperplastic growth; hypertrophic growth; gene therapy; norectic; receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
/note= "1
185..201
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131..152
                                                                                                                                                                                                                                                                                                      /note=
71..89
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52..70
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32..278
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21..42
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1..37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "N-terminal non-transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                           /note-
                                                                                                                                                                           /note=
                                                                                                                                                                                                                             /note=
                                                                                                                                                                                                                                                                              note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Human mature GPCR protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "N-glycosylation site"
                            "Extracellular loop"
                                                                                                                                                                                                                               "Nuclear
                                                                                                                                                                                                                                                                                                                                "Transmembrane domain'
                                                                                                                                                                                                                                                                                                                                                                               "Non-transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Cleavage site for mitochondrial preseq
                                                                           "Transmembrane domain"
                                                                                                                          "Non-transmembrane domain"
                                                                                                                                                                              "Transmembrane domain"
                                                                                                                                                                                                                                                                              "Extracellular loop"
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                                                                                                                                                                                                                             localisation signal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cachexia;
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                                                                                                                                                                                                                                              The invention relates to G protein coupled receptor (GPCR) family commember, 57242 and its corresponding nucleic acid sequence. The 57242 nucleic acid and polypeptide are useful for diagnosing, preventing correcting a subject having or at risk of developing a metabolic disorder, particularly a disorder associated with aberrant lipogenesis or aberrant lipolysis, obesity or diabetes. The 57242 DNA and protein are also useful for treating a subject having bone disorder, where the disorder is osteoporosis or a disorder associated with aberrant correction of the disorder is osteoporosis or a disorder associated with aberrant correction of the disorder is or aberrant bone resorption. These diseases include cobesity, diabetes, hyperlipidaemia, overweight, anorexia or cachexia. The 57242 DNA and protein are also useful for treating a subject having haematopoietic disorders, autoimmune disorders e.g. psoriasis and multiple sclerosis, brain disorders, degenerative diseases e.g. Alzheimer's disease and Pick disease and disorders involving heart. The 57242 DNA cacid and polypeptide are also useful for modulating adipocyte activity such as hyperplastic growth, hypertrophic growth or lipogenesis. The 57242 DNA is used in gene therapy. The present
                                                                                                                                                    Query Match
Best Local
                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human G protein coupled receptor nucleic acid and polypeptide molecules, designated 57242, useful for diagnosing, preventing or molecules, designated 57242 and polypeptide molecules, designated 57242, useful for diagnosing, preventing or molecules, designated for diagnosing, preventing or molecules.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 9;
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   61
               DFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP
DFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP
                                                                                MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA
                                                                MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA
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                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disorders (e.g. osteoporosis)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAD39181
                                                                                                                                                                                                                                       is human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Page 112-113; 114pp; English.
                                                                                                                                                                                                     346
                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001WO-US26882
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216..219
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204..220
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202..220
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281..346
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                                                                                                                                                                                                                                 57242 protein.
                                                                                                                                                 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Nuclear localisation signal"
                                                                                                                                   0;
                                                                                                                               Score 1853; DB 23;
Pred. No. 1.5e-199;
Mismatches 0;
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                                                                                                                                                               Length 346;
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                                                                                                                              Gaps
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RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                 New purinergic-like G-protein coupled receptor AXOR87 polypeptide and polynucleotide, useful for treating diseases related to autoimmunity, inflammation, immunodeficiency, or bacterial, fungal, viral and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                autoimmunity; inflammation; immunodeficiency; bacterial infection; fungal infection; viral infection; protozoa infection; cancer; diabetes; fungal infection; viral infection; protozoa infection; cancer; diabetes; fungal infection; anorexia; bulimia; asthma; psoriasis; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                    Claim 2; Page 36; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                protozoal infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SMIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ignar DM,
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SMITHKLINE BEECHAM PLC
GLAXO GROUP LTD.
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The invention comprises the amino acid and coding sequence of the human purinergic-like 6-protein coupled receptor AXOR87. The AXOR87 DNA and protein sequences of the invention may be used for treating diseases related to immunity, autoimmunity, inflammation, immunodeficiency, and infections (i.e. bacterial, fungal, viral, protozoan). The AXOR87 DNA an protein sequences are particularly useful for treating: cancers, diabetes, obesity, anorexia, bulimia, asthma, psoriasis, rheumatoid arthritis, osteoarthritis, as well as psychotic and neurological disorders. The AXOR87 DNA and protein sequences may also be used as vaccines. The present amino acid sequence (encoded by a sequence located on chromosome 12q24) represents the human AXOR87 protein.

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ABBOLT 7
ABBOLT 7
ABBOLT 6
ABBOLT 7
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This invention relates to a human lipocyte-originated G receptor proteins TGRL3, thought to be antilinflammatory their action. The proteins and encoded DNAs are for use drugs to treat obesity and inflammation, including gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-JUL-2000;
31-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antiinflammatory; anorectic; obesity; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human lipocyte-originated G protein-coupled receptor protein TGR13
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                                                                                                                                Claim 1;
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                                                                                                                                                                             New human lipocyte-originated G protein-coupled receptor proteins TGR13 and encoding DNAs, for developing drugs to treat obesity and inflammations, including gene therapy -
                                                                                                                                                                                                                                                                                                                                                                                                              (TAKE ) TAKEDA CHEM IND LTD.
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                                                                                                                                                                                                                                                    acquired immune deficiency syndrome; inflammatory disorder; infection; Addison's disease; allergy; Grave's disease; metabolic disorder; AIDS; diabetes; obesity; osteoporosis; gene therapy; GCREC-3.
                                                                                                                                                                                                                                                                                       arteriosclerosis; hepatitis; cancer; neurological disorder; epilepsy; Alzheimer's disease; Parkinson's disease; cardiovascular disorder; atherosclerosis; hypertension; myocardial infarction; peptic ulcer; gastrointestinal disorder; dysphagia; anorexia; autoimmune disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE16172 standard;
                                                                                                                                                                                                                                                                                                                                                              Human G-protein coupled receptor 3 (GCREC-3) protein.
                                                                                                                                                                                                                                                                                                                                                                                                             AAE16172;
                                                                       Domain
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                                                                                                                                                                                                        Key
                                                                                                                                                                                                                                                                                                                                      Human; G-protein coupled receptor 3; cell proliferative disorder;
                                                                                                                                                                                                                                                                                                                                                                                      26-MAR-2002
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346; Conserv
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ilarity 100.0%;
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L.5e-199;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CC Parkinson's disease, ataxias, multiple sclerosis, bacterial and viral cardiovascular disorders such as arteriovenous fistula, atherosclerosis, betterial and viral cardiovascular disorders such as arteriovenous fistula, atherosclerosis, cardiovascular disorders such as arteriovenous fistula, atherosclerosis, cardiovascular disorders such as arteriovenous fistula, atherosclerosis, compertensive compertensive infective endocarditis, cardiomyopathy, myocarditis, cardiovenous fistula, atherosclerosis, compertensive compertensive endocarditis, cardiomyopathy, myocarditis, cardiorexia, nausea, peptic ulcer, cholelithiasis, diarriboea, constipation, acquired immune deficiency syndrome (AIDS), hepatic constipation, acquired immune deficiency syndrome, a lergies, spondylitis, amyloidosis, anaemia, asthma, contact compense, allergies, spondylitis, amyloidosis, anaemia, asthma, contact compense, allergies, spondylitis, amyloidosis, anaemia, asthma, contact complysema, grave's disease, gout, multiple sclerosis, rheumatoid compense, systemic lugus erythematosus, uvettis, viral, bacterial, compense, systemic lugus erythematosus, uvettis, viral, bacterial, compense, systemic lugus erythematosus, viral, systemic lugus erythematosus, viral, systemic lugus
                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local 9
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25-MAY-2000;
02-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         coupled receptor 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              also used in gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 myelofibrosis, psoriasis and cancer including adenocarcinoma, leukaemia, lymphoma; neurological disorders such as epilepsy, ischaemic cerebrovascular disease, Alzheimer's disease, Pick's disease, dementia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to human G-protein coupled receptor (GCREC) polypeptides and polynucleotides. GCREC polypeptides are useful for screening compounds that modulate their activity. They are useful in the diagnosis, prevention and treatment of disorders which include the diagnosis, prevention and activity. They are useful includes the diagnosis, prevention and treatment of disorders which include the diagnosis, prevention and treatment of disorders which include the diagnosis.
181 FQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLDSVSAR 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 105-106; 115pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel G-protein coupled receptors and polynucleotides useful for diagnosis, treatment and prevention of disorders of cell proliferation, neurological, cardiovascular, metabolic disorders and viral infections
                                                                                      121
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                                                                                                                                                                                                       DFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120
                                                                                                                                                                                                                                                                                                                          MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA 60
                                                                                                        HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM 180
                                                                                                                                                                                                                                                                             MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA
                                                                              HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM
                                                                                                                                                                               DFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP
                                                                                                                                                                                                                                                                                                                                                                                         346;
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andhi AR,
Lal P, F
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2000US-207566P.
2000US-208834P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      therapy. T
3 (GCREC-3)
                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 1853; DB 23; 100.0%; Pred. No. 1.5e-199;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is human G-protein 3) protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Graul R;
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                                                                                                                                                                                                                                                                                                                                                                            Gaps
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RESULT 9
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                                          Novel isolated polynucleotide, useful for treating infection, pain, cancer, asthma, hypertension, myocardial infarction, urinary retention, osteoporosis, encodes the human HM74-like G-protein coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                              04-APR-2001; 2001WO-EP03811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HM74-like GPCR; G-protein coupled receptor; antibacterial; fungicide; protoxoacide; analgesic; cytostatic; neuroleptic; nootropic; anticonvulsant; tranquilliser; viral infection; pain; cancer; anorexia; bulimia; asthma; central nervous system disease; CNS disease; cardiovascular disease; hypotension; hypertension; angina pectoris; myocardial infarction; urihary retention; osteoporosis; ulcer; asthma; myocardial infarction; urihary retention; osteoporosis; ulcer; asthma;
                                                                                                                                                                         N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                        05-APR-2000; 2000US-194701P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W0200177320-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               inflammation; allergy; benign prostatic hypertrophy; multiple sclerosis; psychotic disorder; neurological disorder; dyskinesia; Huntington's disease; Tourette's syndrome; anxiety; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU11401 standard; Protein; 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HM74-like G-protein coupled receptor (GPCR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-FEB-2002
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                                                                                                                                                                      2002-049147/06.
DB; AAS18501.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          depression; delirium; dementia; mental retardation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "G-protein coupled receptor region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= Transmembrane_domain_7
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polypeptide

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Claim 1; Fig 2; 77pp; English.
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ulcer, asthma, inflammation, allergy, benign prostatic hypertrophy, multiple sclerosis and dyskinesia such as Huntington's disease and Tourette's syndrome. The composition is also useful for treating psychotic and neurological disorders such as anxiety, schizophrenia, manic depression, delirium, dementia and severe mental retardation. (I) or the HM74-like GPCR polypeptide are also useful for treating the above mentioned diseases. (I) is useful in a diagnostic assay for detecting diseases, susceptibility to diseases and abnormalities related to the presence of mutations in the nucleic acid sequences which encode a GPCR. The polypeptide is useful to identify test compounds which may act as agonists or antagonists at the receptor site and which can be regulated to provide therapeutic effects. The polypeptide is also useful as a bait production of polycional antibodies. This the amino acid sequence of The invention describes a novel isolated polynucleotide (I) encoding a human HM74-like G-protein coupled receptor (GPCR) polypeptide. Reagents that regulate HM74-like GPCR are useful for modulating the activity of the protein in a disease selected from bacterial, fungal, protozoan, and viral infection, pain, cancer, anorexia, builmia, asthma, central nervous system (CNS) disease, cardiovascular disease, hypotension, hypertension, angina pectoris, myocardial infarction, urinary retention, osteoporosis, human HM74-like GPCR described in the method of the invention.

Sequence 346 AA;

Query Match

Length 346;

Дb 밁 Qγ 밁 δÃ В δÃ B γ QΥ Ωy Matches 301 181 181 121 121 61 61 Loca _ 1 MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA 60 QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDPHIVEWH 346 QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDPHIVEWH HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM 180 DFLLMICLPFRTDYYLRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP DFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120 ${\tt MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA}$ LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK FQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR FQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM Similarity Conservative 100.0%; 0 Score 1853; DB 23; Pred. No. 1.5e-199; Mismatches 0, Indels 0; Gaps 300 60 0,

AAE17077 standard; Protein; 346 AA

18-APR-2002 (first entry)

Human G-protein coupled receptor (GPCRx14) protein.

RESULT 10
AAE17077
ID AAE17
XX AAE17
AC AAE17
XX 18-AP
DT 18-AP
XX Human
XX Human
KW receg
KW ostec
KW anore
KW anore
KW depre
KW Alzhe osteoporosis; angina pectoris; restenosis; atherosclerosis; hypotension; anorexia; tumour; migraine; acute heart failure; ulcer; antiinflammatory; stroke; hypertension; neuronal disorder; myocardial infarction psychotic; depression; mental retardation; neurodegenerative disease; antibacterial; Human; G-protein coupled receptor; GPCRx14; cerebroprotective; vomiting; receptor-mediated disorder; therapy; urinary retention; allergy; obesity; Alzheimer's dementia; ischaemia; Parkinson's disease;

Huntington's disease; anxiety; antifungal; immunosuppressive; cytostatic; vulnerary; analgesic; anorectic; anabolic; diuretic; cardiant; nootropic; antiemetic; vasotropic; diabetes; cancer; tranquillizer; neuroleptic.

Key Domain Domain Doma in Doma in Domain Domain Domain /note= 52..70 Location/Qualifiers 17..40 /note= 185..2 /note= 258..28 /note= 221..2 /note= /note= note= . 281 . 237 . 203 "Transmembrane domain" "Transmembrane domain" "Transmembrane domain" "Transmembrane domain" "Transmembrane domain" "Transmembrane "Transmembrane domain"

WO200198330-A2

27-DEC-2001

20-JUN-2001; 2001WO-BE00104

11-JUL-2000; 26-JAN-2001; 20-JUN-2000; 2000US-212913P 12-FEB-2001; ; 2000US-217494P. ; 2001EP-0870015. ; 2001EP-0870024.

(EURO-) EUROSCREEN SA

Brezillon Detheux M, Parmentier M, Govarts

Ç

N-PSDB; AAD27497. 2002-130789/17.

medicaments New G-protein coupled receptor, useful in the manufacture of failure and for treating receptor mediated disorders e.g. acute heart ${\tt Alzheimer}$'s disease -

Disclosure; Page 29; 46pp; English.

urinary retention, osteoporosis, angina pectoris, atherosclerosis, restenosis, diseases involving excessive or reduced proliferation or loss of smooth muscle cells, aneurysm, stroke, ischaemia, ulcers, allergies, benign prostatic hypertrophy, migraine, vomiting; blood circulating affections including acute heart failure, hypotension, hypertension and myocardial infarction psychotic; neuronal disorders such as anxiety, schizophrenia, maniac depression, depression, delirium, dementia, severe mental retardation; degenerative diseases; neurodegenerative diseases such as Alzheimer's disease, Parkinson's disease; and dyskinesias e.g. Huntington's disease or Gilles de la Tourette's syndrome and other related diseases. The present sequence is GPCRx14 protein. nucleotide encoding it. GPCR are useful in the manufacture of a medicament for the prevention and/or treatment of receptor-mediated disorders e.g. viral infections, virus and bacterial diseases diseases and disorders involving disturbances of cell migration, diseases or perturbations of immune system including cancers, development of tumours perturbations of immune system including cancers, development of tumours and tumour metastasis, inflammatory and neoplastic processes; bac and fungal infections, in wound and bone healing, dysfunction of The present invention relates to a G-protein coupled receptor (GPCR) and regulatory growth functions; pains, diabetes, obesity, anorexia, bulimia bacterial

Sequence

Query Match Best Local Matches 346; Similarity Conservative 100.0%; 0; Score 185 Pred. No. Mismatches 1853; 1.5e-199 DΒ Indels Length 346; 0; Gaps

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RESULT 11
ABB44523
ID
ABB44523
AC
ABB44
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                                                                                                                                                                                                                                                  06-APR-2000;
21-JUL-2000;
27-JUL-2000;
27-JUL-2000;
28-JUL-2000;
11-AUG-2000;
11-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                   06-APR-2000;
06-APR-2000;
06-APR-2000;
06-APR-2000;
06-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  anabolic; cytostatic; antiviral; gene therapy; cardiomyopathy; obesity; anorexia; diabetes; osteoporosis; Crohn's disease; multiple sclerosis; asthma; Alzheimer's disease; Parkinson's disorder; Huntington's disease;
       Majumder K,
Padigaru M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAR-2001; 2001WO-US10241
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                                                                             (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                             18-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDPHIVEWH 346
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                                                                                                                                                                                                                                                                            2000US-221284P.
2000US-221325P.
2000US-224588P.
       Vernet CAM,
Mishnu VS,
                                                                                                                                                                            2001US-263433P
2001US-263604P
                                                                                                                              2001US-265161P
2001US-0823172
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2000US-195510P.
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2000US-195069P.
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2000US-195067P.
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     Tchernev
     Casman SJ,
Tchernev VT,
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Wolenc AR,
Spytek KA,
  Spaderna SK
Li L;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CC (GPCRX) polypeptides. The polypeptides have potential cardiant, and antivital activity. The CC antiarteriosclerotic, anabolic, cytostatic and antivital activity. The CC polypeptides can be administered therapeutically, especially using gene CC therapy and expressing the encoding DNA in vivo, to treat or prevent CC GPCRX-associated disorders, especially in humans. For example, they can CC be used to treat/prevent cardiomyopathy, atherosclerosis, disorders CC related to signal processing and metabolic pathway modulation (e.g. CC obesity, anorexia), diabetes, osteoporosis, Crohn's disease, multiple CC sclerosis, asthma, cancers, neurodegenerative disorders (e.g. Alzheimer's CC disease, Parkinson's disorder, Huntington's disease), immune disorders, certain the presence of or predisposition to a disease associated CC with altered levels of the polypeptide in mammals (especially humans) by CC detecting alterations in polypeptide expression levels relative to cellular receptors or downstream effectors) and/or agents modulating cellular polypeptide expression or activity, useful as cc antagonists and agonists in disease treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to nucleic acid sequences (ABA81529-ABA81552) that encode G-coupled protein-receptor related polypeptides (ABB4522-ABB44543). The isolated polypeptide having a sequence differing by no more than 15% of amino acid residues from one of 22 amino acid sequences (or mature forms of the sequences), fully defined in the specification and corresponding to human G-protein coupled receptor X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New human G-protein coupled receptor X, GPCRX, polypeptide useful in treatment or prevention of GPCRX associated disorders e.g. cardiomyopathy or atherosclerosis, and to screen for antagonists and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      agonists useful therapeutically
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                                                                                                  LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK
QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDPHIVEWH
                                     QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDPHIVEWH 346
                                                                              LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK
                                                                                                                                                                                       FQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR
                                                                                                                                                                                                                                                                                                                                                    DFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120
                                                                                                                                                               FQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR
                                                                                                                                                                                                                                               HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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Pred. No. 5.6e-198;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 346;
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RESULT 12 AAG80934

AAG80934 standard; Protein; 296

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28-DEC-1999
22-FEB 2000
28-FEB-2000
28-FEB-2000
02-MAR-2000
03-MAR-2000
03-MAR-2000
17-MAR-2000
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                                                                                                           The present invention relates to novel G protein-coupled receptors (nGCPCRx; where x is 1, 3, 4, 5, 9, 11, 12, 14-18, 20, 21, 22, 24, 27, 28, 31-38, 40, 41, 53-60) and their coding sequences. The present sequence is one such G protein-coupled receptor. GPCRs are also known as seven transmembrane receptors and function in signal transduction. The nGPCRx coding sequences are useful for screening a human to diagnose a disorder affecting the brain or a genetic predisposition, specifically schizophrenia. nGPCRx are useful for identifying compounds useful for treating schizophrenia. Detection of nGPCRx in a sample is useful as a diagnostic tool for diseases or disorders e.g. thyroid disorders, renal failure, rheumatoid arthritis, CNS disorders, infections such as HIV-1, metabolic and cardiovascular diseases.
and neuronal disorders such as Alzheimer's disease, Parkinson's disease migraine and senile dementia. Additional disorders include inflammatory conditions (e.g. Crohn's disease), rheumatoid arthritis, autoimmune
                                                                                                                                                                                                                                                                                                                       Claim
                                                                                                                                                                                                                                                                                                                                                    New G protein-coupled polynucleotide useful
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       attention deficit-hyperactivity disorder/attention deficit disorder; Parkinson's disease; migraine; senile dementia; inflammatory disease;
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                                              metabolic and cardiovascular diseases, proliferative disorders and hormonal disorders. Modulators of nGPCRx activity have the utility for treating neurological disorders, including schizophrenia, ADHD/ADD (attention deficit hyperactivity disorder/attention deficit disorder).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (PHAA ) PHARMACIA & UPJOHN CO.
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                                                                                                                                                                                                                                                                                                                                                                                                                      2001-389826/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     KA,
                                                                                                                                                                                                                                                                                                                     Pages 77-78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wood
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2000US-0185421
2000US-018554
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2000US-0186811
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PS, Banni
                                                                                                                                                                                                                                                                                                                                                    receptor (nGPCR-x)
for diagnosing and
                                                                                                                                                                                                                                                                                                                    261pp; English.
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an CM, Ruff V,
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V, Sejlitz
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                                Parkinson's disease
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Huff RM;
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                                                                                                                                                                                                                                                                                                                                                                                                                Human; inflammation-associated G-protein coupled receptor; GPCR; EX20; inflammatory disease; asthma; adult respiratory distress syndrome; ARDS; chronic obstructive pulmonary disease; GOPD; bronchitis; emphysema; pneumoconiosis; neutrophll; eosinophil related disorder; airway; lung-related disorder; rheumatoid arthritis; inflammatory bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disorders, cancers, respiratory ailments such as asthma, and inflammatory diseases e.g. inflammatory bowel disease.
                             Claim 2;
                                                                   New pharmaceutical composition comprising EX20 polypeptide, EX20 polynucleotide, antibodies against EX20 polypeptide, antisense oligonucleotides against EX20 polynucleotide, useful for treating
                                                                                                                                                                                                         SAON)
                                                                                                                                                                                                                                                     18-AUG-2000; 2000US-0641653.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human inflammation-associated GPCR EX20 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU77992 standard; Protein;
                                                                                                                                                                             Jarai
                                                                                                                                                                                                                                                                                 16-AUG-2001; 2001WO-EP09466
                                                                                                                                                                                                                                                                                                              21-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                  ulcerative colitis;
                                                                                                                                N-PSDB; ABK47759.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 LLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMICLPFRTDYYLRRRH 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIMFQLEFFMPLGIILFCSFKIV 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WAFGDIPCRYGLETLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVAAGIVCTLW 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPKQPGHSKTQRPEEMPIS 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSARLYFLWTVPSSACDPSVHGAL 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVAAGIVCTLW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMICLPFRTDYYLRRRH
                                                                                                                                                2002-329542/36.
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                                                                                                                                                                             G,
                                                                                                                                                                                                       ) NOVARTIS AG.
) NOVARTIS-ERFINDUNGEN
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                             Page
                                                                                                                                                                             Yousefi S;
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                             31-32;
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                                                                                                                                                                                                                                                                                                                                                                                                  skin disease; eczematous dermatitis; receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84.7%;
100.0%;
                             36pp;
                             English
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                                                                                                                                                                                                            VERW GES
to human inflammation-associated
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Best Local
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      Bergsma DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  G-protein coupled receptor HM74A protein.
                                                                                                                                12-JUN-1997;
                                                                                                                                                                                                                                                                 17-DEC-1998
                                                                                                                                                                                                                                                                                                                                  W09856820-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                        asthma; allergy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HM74A receptor; G-protein coupled receptor; infection; pain; cancer; diabetes; obesity; neurological disorder; heart failure; hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-APR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW94654 standard; Protein; 363
                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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                                                                (SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                 12-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WTVPSSA---CD--PSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKP
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Elshourbagy NA,
                                                                                                                                97US-0049480
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52.88;
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Pred. No. 5.3e-92;
Guerrera SF,
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Li X,
Mooney JL;
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Human G-protein coupled receptor,

hRUP25

23-OCT-2001

(first entry)

Homo sapiens

Human; G-protein coupled receptor; GPCR; hRUP25; agonist; inverse agonist; lung cancer. AAU04379

AAU04379 standard; Protein; 363 AA

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RESULT 15
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 acute heart failure, hypotension, hypertension, urinary retention, osteoporosis, angina pectoris, myocardial infarction, stroke, ulcers, asthma, allergies, benign prostatic hypertrophy, migraine, vomiting, psychotic and neurological disorders, including anxiety, schizophrenia, manic depression, depression, delirium, dementia, and severe mental retardation, and dyskinesias such as Huntington's disease or Gilles de la Tourett's syndrome. The products can also be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is a member of the G-protein coupled receptor (7TM receptor) family, designated the HM74A receptor. The proteins, agonists, antagonists and polynucleotides can be used for treating disorders associated with increased or reduced expression or activity of HM74A, e.g. bacterial, fungal, protozoan and viral infections, particularly infections caused by HIV-1 or HIV-2, pain, cancers, diabetes, obesity, anorexia, bulimia, asthma, Parkinson's disease, acute heart failure broatension becaute failure broatension.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated G-protein coupled receptor, HM74A - used to develop products for treating e.g. infections, pain, cancers, diabetes, obesity, neurological disorders, heart failure, hypertension, asthma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       detection,
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N-PSDB; AAX16671.
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                                                                                                                                                                                                                                              FEMPLGIILECSEKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSARLYFL
                                                                                                                                                                                                                                                                                                                                                                                                            MICLPFRTDYYLRRRHWAFGDIPCRVGLETLAMNRAGSIVFLTVVAADRYFKVVHPHHAV 124
                                                                                                                                                                             WTVPSSA---CD--PSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKP
                                                                                                                                                                                                                      FFLPLGIILFCSARIIWSLRQR-QMDRHAKIKRAITFIMVVAIVFVICFLPSVVVRIRIF 255
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                                                                                                                                                                                                                                                                                                                                                                                      IICLPFLMDNYVRRWDWKFGDIPCRLMLFMLAMNRQGSIIFLTVVAVDRYFRVVHPHHAL
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                                                        KMTGEPDNNRSTSVELTGDPNKT-RGAPEALMANSGEPWSP 355
                                                                                                                                        WLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPSFPNFFSTLINRCLQR 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47.7%; Score 883.5; DB 2 52.8%; Pred. No. 1.8e-90;
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                                                                                                                                                                                                                                                                                                                        The sequence represents a human G-protein coupled receptor (GPCR), hRUP25. The endogenous and non-endogenous, constitutively activated versions of human G-protein coupled receptors (GPCR), are useful for direct identification of candidate compounds as receptor agonists, inverse agonists or partial agonists having applicability as therapeutic agents for treating diseases related to GPCR, e.g. lung cancer. Non-endogenous version of human GPCRs are also utilized in research settings and in vitro and in vivo system, incorporating GPCRs can be utilised to elucidate and understand the roles these receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Endogenous and non-endogenous versions of human G-protein coupled receptors for direct identification of candidate compounds as agonists, inverse agonists or partial agonists for use as therapeutic agents -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 69; Page 121-122; 160pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-355616/37.
N-PSDB; AAS07952.
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17-NOV-1999;
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                                                                                                                                                                                                                                                                                                              play in the human condition, both normal and diseased.
77
                                                                                                                             65 MICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAV 124
                                                                                                                                                                      17
                                                                                                                                                                                      5 SCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLL 64
                                                                                                                                                                      NCCVFRDDFIVKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWKSSRIFLFNLAVADFLL 76
                                                         NKISNRTAAIISCLLWGITIGLTVHLLKKKMPIQNGGANLCSSFSICHTFQWHEAMFLLE
                                                                      NTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIMFQLE 184
                                                                                                                 IICLPFLMDNYVRRWDWKFGDIPCRLMLFMLAMNRQGSIIFLTVVAVDRYFRVVHPHHAL 136
                                                                                                                                                                                                                                           Similarity
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99US-0171902

200US-0181749

2000US-0189258

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2000US-020619
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2000US-0210982.
2000US-0226760.
2000US-0235418.
2000US-0235779.
2000US-0242332.
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                                                                                                                                                                                                                                          47.7%; Score 883.5; DB 22; 52.8%; Pred. No. 1.8e-90;
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                                 KMTGEPDNNRSTSVELTGDPNKT-RGAPEALMANSGEPWSP 355
                 KQPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDP
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Search completed: March Job time : 77 secs 26, 2003, 19:37:33

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Result
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Maximum DB seq
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Perfect score:
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       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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US-08-955-713-2 US-08-955-713-2 US-08-955-713-2 Sequence 2, Application US/08955713 Patent No. 5955308 GENERAL INFORMATION: APPLICANT: BATHE, GANESH APPLICANT: BERGSMA, DERK APPLICANT: BERGSMA, DERK APPLICANT: HALSEY, WENDY TITLE OF INVENTION: CDNA CLONE HEOAD54 THAT ENCODES TITLE OF INVENTION: ADDRESS: ADDRESSEE: RATMER & PRESTIA SCHERET: PA COUNTRY: USA COUNTRY: USA COUNTRY: USA ZITP: 19482 COMPUTER READABLE FORM: MEDIUM TYPE: Diskettle COMPUTER: IBM COMPATIBLE COMPUTER: DATA: MEDIUM TYPE: Diskettle COMPUTER: IBM COMPATIBLE COMPUTER: STATES FORM: CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/955,713 FILLING DATE: 23-007-1997 CLASSIFICATION NUMBER: US/08/955,713 REFERENCE/DOCKET NUMBER: G0/050,124 FILLING DATE: 18-JUN-1997 ATTOKNEY/AGENT INFORMATION: NAME: PRESTIA, PAUL F REGISTRATION NUMBER: 23-031 REFERENCE/DOCKET NUMBER: G1-70087 TELEFAX: 610-407-0701 TELEX: 84-6169 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTFERISTICS: LENGTH: 423 amino acids TYPE: amino acids TYPE: minio acids TYPE: minio acids TYPE: minio acids TYPE: DATOKET TYPE: DYTOKEN NOLECULE TYPE: DYTOKEN US-08-955-713-2	ALIGNMENTS	28 307 16.6 395 2 US-08-476-976-5 29 307 16.6 395 3 US-08-477-410-5 30 306 16.5 398 1 US-08-097-938-6 31 306 16.5 398 1 US-08-472-840-6 32 306 16.5 398 1 US-08-476-976-6 33 306 16.5 398 2 US-08-476-976-6 34 306 16.5 398 3 US-08-474-410-6 35 305.5 16.5 398 3 US-08-170-601B-9 37 305.5 16.5 391 1 US-08-112-0601B-9 38 305.5 16.5 391 1 US-08-417-103-14 40 305.5 16.5 391 1 US-08-417-103-14 40 305.5 16.5 391 1 US-08-417-103-14 40 305.5 16.5 391 1 US-08-417-103-14 41 303.5 16.3 369 1 US-08-417-103-6 42 302.5 16.3 369 1 US-08-417-103-6 43 302.5 16.3 369 1 US-08-417-103-6 44 302.5 16.3 369 1 US-08-417-103-6 45 302 16.3 369 1 US-08-417-103-6
A HUMAN 7-TRANS		Sequence 5, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 2, Appli Sequence 2, Appli Sequence 14, Appli Sequence 2, Appli Sequence 3, Appli Sequence 6, Appli Sequence 16, Appli Sequence 16, Appli

Query Match
Best Local Similarity
Matches 115; Conserv

Conservative

48;

Score 529; DB 2; 1 Pred. No. 3.9e-38; 8; Mismatches 108;

Length 423; Indels

22;

Gaps

7;

28.5%;

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; MOLECULE TYPE: US-08-955-713-4
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                                                                                                                                                                                                      TELEX: 846169
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                     FILING LANGE 435
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/050,124
APPLICATION NUMBER: 18-JUN-1997
                                                                                                                                                                                                                                                           NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
                                                                                                                                                                                     SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: CDNA CLONE HEOAD54 THAT ENCODES NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 18-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         141 LISNLPLRVDYYLLHETWRFGAAACKVNLFMLSTNRTASVVFLTAIALNRYLKVVQPHHV 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         314 FGMASMVAFWLSACRSLDLCTQLFHG----SLAFTYLNSVLDPVLYCFSSPNF 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          238 --SARLYFLWTVPSSA----CDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSF 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              255 ALYLLEFFLPLALILFAIVSIGLTIRNR-GLGGQAGPQRAMRVLAMVVAVYTICFLPSII 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 179 IMFQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSV- 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  201 LSRASVGAAARVAGGLWVGI-----LLLNGHLLLSTFSGPSCLSYRVGTKPSASLRWHQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124 VNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQE-TAVSCESFIM----ESANGWHD 178
                                                                                                                              STRANDEDNESS:
                    Local Similarity
                                                                                                                 TOPOLOGY:
                                                                                                                                                     TYPE:
                                                                                                                                                                                                                                            TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/955,713 FILING DATE: 23-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 LMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHA 123
                                                                                                                                                                    LENGTH:
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                                                                                                                                               amino acid
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BERGSMA, DERK
HALSEY, WENDY
                                                                                                                                                                  476 amino acids
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   Conservative
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O. BOX 980
                                                                                              protein
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                                                                                                                                single
                  27.5%; Score 510; DB 2; 39.6%; Pred. No. 1.9e-36;
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47; Mismatches
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101;
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20;
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Gaps
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SEQUENCE DESCRIPTION: SEQ ID NO: US-09-130-749-2
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      Matches 101;
                          Query Match
Best Local :
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                                                                                                                                                                                                                         TELEX: 846169
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      240 SLDLCTQLFHG----SLAFTYLNSVLDPVLYCFSSPNF 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 FAIVSIGLTIRNR-GLGGQAGPQRAMRVLAMVVAVYTICFLPSIIFGMASMVAFWLSACR 239
                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         251 A---CDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSF 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             126 GIWYGILLLNGXLLLNTF-----SGPSCLSYRYGTKPSASLRWHQALYLLEFFLPLALIL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  138 TLWALVILGTVYLLLENHLCVQETAVSCESFIM----ESANGWHDIMFQLEFFMPLGIIL 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66 HETWRFGAAACKVNLFMLSTNRKASVVFLTAIALNRYLKVVXPHHVLNRASVGAXARVXG 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78 RRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVAAGIVC 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18 MPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMICLPFRTDYYLR
                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: GP-70513 TELECOMMUNICATION INFORMATION: TELEPHONE: 610-407-0700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/130,749
FILING DATE: 07-Aug-1998
CLASSIFICATION: UNKNOWN
                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: SHABON, USMAN ELSHOURBAGY, NABIL
                                                                                                                            MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: MOLECULAR CLONING OF A 7TM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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                                                                                                                                                                 STRANDEDNESS: single
                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: <Unknown> FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
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                                                                                                                                            TOPOLOGY:
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                                                                                                                                                                                                          LENGTH: 319 amino acids
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      Conservative
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                      24.4%;
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  61;
Score 451.5; DB 3;
Pred. No. 1.4e-31;
1; Mismatches 121;
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                                         Length 319;
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                                                                     Matches 101;
                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: GP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: RATNER & PRESTIA
STREET: P.O. Box 980
                                                                                                                                                          MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          183 CLQFVLPFGLIVFCNAGIIRALQKRLREPEKQPKLQRAQALVTLVVVLFALCFLPCFLAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    243 VLMHIFQNLGSCRALCAVAHTSDVTGSLTYLHSVLNPVVYCFSSPTFRSSYRRV 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 -- LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKL 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          182 QLEFFMPLGIILFCSFKIVWSLRRR-QQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                126 LSPQAALGVSGLVWLLMVALTCPGLLISE--AAQNSTRCHSF-YSRADGSFSIIWQEALS 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    127 ISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANG-----WHDIMF 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: UZIP: 19482
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CITY: Valley Forge
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67 CLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09 FILING DATE: 07-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM:
                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                             NAME: PRESTIA, PAUL F
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE:
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                                CRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMI 66
CSAPSTVVATAVGVLLGLECGLGLLGNAVALWTFLFRVRVWKPYAVYLLNLALADLLLAA 65
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VENTION: MOLECULAR CLONING OF A
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                                                                     Conservative
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                                                                                    24.48;
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                                                                     61; Mismatches 121;
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                                                                                      Score 451.5;
Pred. No. 1.4
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                                                                                                                                                                                                                                                                                                              FILING DATE: 19-AUG-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 14-SEP-199
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Ohgi, Kazuhiro
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
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APPLICATION NUMBER:
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                                    FILING DATE: 30-SEP-PRIOR APPLICATION DATA:
                                                                                       FILING DATE: 02-NOV-PRIOR APPLICATION DATA:
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                                                                                                                                             PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 --LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKL 292
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APPLICATION NUMBER: JP 6 FILING DATE: 30-SEP-1994
                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 16-MAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/JP95/01599 FILING DATE: 10-AUG-1995
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                                                                        APPLICATION NUMBER:
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                                                                                                                                                                                 APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLPFLAAFYLSLQAWHLGRYGCWALRFLLDLSRSYGMAFLAAVALDRYLRVYHPRLKVNL 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LSPQAALGVSGLVWLLMVALTCPGLLISE--AAQNSTRCHSF-YSRADGSFSIIWQEALS 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANG-----WHDIMF 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Floppy disk
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                     JP 6-236356
                                                                        JP 6-236357
                                                                                                                              JP 6-270017
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                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/08559524A Patent No. 5871963
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                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Conley, Pamela B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 374;
                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                APPLICANT: Conley, Pamela B.
APPLICANT: Jantzen, Hans-Michael
TITLE OF INVENTION: NOVEL PURINERGIC RECEPTOR
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 362 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 617-523-3400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        292 LKICSLKPKQPGHSKTQRPEEMPISNL 318
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COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                              COUNTRY:
                                                                                                                    STATE:
                                                                                                                                                       STREET:
                                                                                                                                                                       ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: JP 6-189272 FILING DATE: 11-AUG-1994
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FILING DATE: 11-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                     ATRKSSRRSEP--NVQSKSEEMTLNIL 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TLWALVILGTVYLLLENHL------CVQETA------VSCESFIMESANGWHD 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----SVSARLYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNK 291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IMFQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLP--- 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVAAGIVC 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MKTLNLRARLDF-QTPQMCAFNDKVYATYQVTRGLASLNSCVDPILYFLAGDTFRRRLSR 326
                                                                                                                               Washington
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                                                                                                                                                   1800 M Street, N.W.
                                                                                                USA
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US-08-749-707-4
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GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                 SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                              APPLICANT: Conley, P
APPLICANT: Jantzen,
TITLE OF INVENTION:
                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 202-467-7000
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LENGTH: 373 amino acids
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 APPLICATION NUMBER:
                                                                                                                                                   COUNTRY:
                                                                                                                                                                         STATE:
                                                                                                                                                                                       CITY: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Adler, Reid G. REGISTRATION NUMBER: 30,988
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 044481-5010-00-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/559,524A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MPPLLIVAFVLGALGNGVALCGECEHMKTWKPSTVYLFNLAVADELLMICLPERTDYYLR 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --ATRKASRRSEANLQSKSEDMTLNILSEFKQNGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LDF-QTPEMCAFNDRVYATYQVTRGLASLNSCVDPILYFLAGDTFRRRLSR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLP-----SVSAR 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LVWLIVVVGISPILFYSGTGIRKNKTITCYDTTSDEYLRSYFIYSM-----CTTVAMFCV 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TLWALVILGTVYLLLENHLCVQET-AVSC-----ESFIMESANGWHDIMFQLEFFM 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVAAGIVC 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PLVLILGCYGLIVRALIYK-DLDNSPLRRKSIYLVIIVLTVFAVSYIPFHVMKTMNLRAR 287
                                                                                                                                    20036-5869
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92; Conserv
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                                                                                                                                                                                                         E: MORGAN, LEWIS & BOCKIUS LLF 1800 M Street, N.W.
                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                         Conley, Pamela B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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                                                                                                                                                                                                                                                                                 Hans-Michael
NOVEL PURINERGIC RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19.6%; Score 362.5; DB 2 27.5%; Pred: No. 7.9e-24;
US/08/749,707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 373;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No. 6010877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Sathe, Ganesh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: protein
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NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Sathe, Ganesh
APPLICANT: Van Horn, Stephanie
APPLICANT: Bergama, Derk
APPLICANT: Mao, Joyce Yue
TITLE OF INVENTION: CDNA CLONE HE8CS41 THAT ENCODES A NOVEL 7-TRANSMEMBRAN
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 373 amino acids
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                                                       OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham
                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSD 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   188 PLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLP-----SVSAR 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    174 LVWLIVVVGISPILFYSGTGIRKNKTITCYDTTSDEYLRSYFIYSM-----CTTVAMFCV 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 138 TLWALVILGTVYLLLENHLCVQET-AVSC------ESFIMESANGWHDIMFQLEFFM 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 114 KTDWIFGDAMCKLQRFIFHVNLYGSILFLTCISAHRYSGVVYPLKSLGRLKKKNAVYISV 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 709 Swedeland CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: SWEDELAND SWEDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78 RRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVAAGIVC 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54 LPAVYILVFIIGFLGNSVAIWMFVFHMKPWSGISVYMFNLALADFLYVLTLPALIFYYFN 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18 MPPLLIVAFYLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMICLPFRTDYYLR 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
wes 92; Conserv
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                                                                                                                                                                                                   COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --ATRKASRRSEANLQSKSEDMTLNILSEFKQNGD 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LDF-QTPEMCAFNDRVYATYQVTRGLASLNSCVDPILYFLAGDTFRRRLSR-----
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                                                                                                                                                                                                                                                                                                                          19406
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                                                                                                                                                                                           IBM Compatible
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                                                                                                                                                                                                                                         Diskette
10-JAN-1997
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27.5%;
                                      US/08/781,250
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                                                                                                                                                                                                                                                                                                                                                                                      RESULT 9
US-08-153-848-44
                                                                                                                                                                                                                                                                                                                                                  Sequence 44, Application US/08153848 Patent No. 5759804
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: 610-270-5219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                 APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: No. 5759804el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    336 TETP 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             143 VILGTVYLLLENHLCVQETAVSC-ESFIMESANGWHDIMFQLE-----FFMPLGIILF 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
TYPE: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24 VAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMICLPFRTDYYLRRRHWAF 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
               COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                        COUNTRY:
                                                                                                                                             STREET: 6300 S
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84 GDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVAAGIVCT-LWAL 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48 VVFILGLITNSVSLFVFCFRMKMRSETAIFITNLAVSDLLFVCTLPFKI-FYNFNRHWPF 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 610-270-4060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                  ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Bicknell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TNCFLERFAKIMYPITLCLATLNCCFDPFIYYFTLESFQKSFYINAHI-----RMESLFK 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CSSVVLRTLRKPATLSQIGTNKKKVLKMITVHMAVFVVCFVPYNS--VLFLYALVRSQAI 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CSFKIVWSLRRRQQLAR-QARMKKATRFIMVVAIVFITCYLPSVSARLYFLWTVPSSAC- 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GDTLCKISGTAFLTNIYGSMLFLTCISVDRFLAIVYPFRS-RTIRTRRNSAIVCAGVWIL 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TQRP 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----DPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPK-FYNKLKICSLKPKQPGHSK 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VLSGGISASLFSTTNVNNATTTCFEGF---SKRVWKTYLSKITIFIEVVGFIIPLILNVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95;
                                                                                             60606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
                                                                                                                              Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   370 amino acids
                                                                                                                                                                   6300 Sears Tower,
                                                                                                            USA
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             IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
 PatentIn Release #1.0,
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31.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52; Mismatches 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATG50043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 346.5; DB 3
Pred. No. 1.9e-22;
                                                                                                                                                                   233 South Wacker Drive
Version
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   #1
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                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/08812871 Patent No. 5955303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 514
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/977,452
FILLING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5759804and, Greta E.
REGISTRATION NUMBER: 35,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                          APPLICANT: Au-Young, Janice
APPLICANT: Guegler, Karl
APPLICANT: Guegler, Karl
APPLICANT: Muzong Cheng
TITLE OF INVENTION: NOVEL HUMAN CHEMOKINE RECEPTOR-LIKE
TITLE OF INVENTION: PROTEIN
                  COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEPAX: (312) 474-0448
TELEX: 25-3856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:

ADDITICATION NUMBER: US/08/153,848
                                                                                                                                                                                                                                                                                                                                                                                                                                                      317 LKGPPPSFEGKTNESSLS 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 242 YFL-WTVPSSACDPSVHGAL--HITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLK 298
  COMPUTER:
                                                                           COUNTRY:
                                                                                                     STATE:
                                                                                                                                     STREET:
                                                                                                                                                        ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PKQPGHSKTQRPEEMPIS 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EFFMPLGIILFCSFKIVWSLRRRQQLARQARMK-KATRFIMVVAIVFITCYLP-SVSARL 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ISTR--VAAGIVCT-LWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIMFQL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VLPTRLVYHFSGNHWPFGEIACRLTGFLFYLNMYASIYFLTCISADRFLAIVHP---VKS 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLPFRTDYYLRRRHWAEGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YVLHYRSHGASCATQRILALANRITSCLTSLNGALDPIMYFFVAEKFRHALCNL-LCGKR 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AFTFPFITTVTCYLLIIRSL--ROGLRVEKRLKTKAVRMIAIVLAIFLVCFVPYHVNRSV 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LKLRRPLYAHLACAFLWVVVAVAMAPLLVSPQTVQTNHTVVCLQLYREKASHHALVSLAV 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGQETPLENMLFASFYLLDFILALVGNTLALWLFIRDHKSGTPANVFLMHLAVADLSCVL 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 Similarity
97; Conserv
                                                          94304
                                                                                                               Palo Alto
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                                                                                               CA
                                                                                                                                     3174 Porter Dr.
                                                                               USA
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IBM Compatible
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                                                                                                                                                        Incyte Pharmaceuticals,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18.1%; Score 336; DB 1; Lot 30.5%; Pred. No. 1.4e-21; ative 54; Mismatches 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44:
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                                                                                                                                                                                                                                   Sequence 44, Application US/09299843A Patent No. 6107475
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 97; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 415-845-4166 INFORMATION FOR SEQ ID NO:
                                                                                                                                     APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                               APPLICANT: Godiska, Ronald APPLICANT: Gray, Patrick W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IMMEDIATE SOURCE:
LIBRARY: GenBa
CLONE: 992700
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: Filed Herewith PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                     317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        140 LKLRRPLYAHLACAFLWVVVAVAMAPLLVSPQTVQTNHTVVCLQLYREKASHHALVSLAV 199
                                                                                                                                                                                                                                                                                                                                                                                                                        299 PKQPGHSKTQRPEEMPIS 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 242 YFL-WTVPSSACDPSVHGAL--HITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLK 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           200 AFTFPFITTVTCYLLIIRSL--ROGLRVEKRLKTKAVRMIAIVLAIFLVCFVPYHVNRSV 257
                                   STREET: 6300;
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             127 ISTR--VAAGIVCT-LWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIMFQL 183
COUNTRY:
                STATE:
                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83 VLPTRLVYHFSGNHWPFGEIACRLTGFLFYLNMYASIYFLTCISADRFLAIVHP---VKS 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67 CLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23 CGQETPLENMLFASFYLLDFILALVGNTLALWLFIRDHKSGTPANVFLMHLAVADLSCVL 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Billings, Lucy J
REGISTRATION NUMBER: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 CRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMI 66
                                                                                                                                                                                                                                                                                                                                                                                   LKGPPPSFEGKTNESSLS 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                              YVLHYRSHGASCATQRILALANRITSCLTSLNGALDPIMYFFVAEKFRHALCNL-LCGKR 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EFFMPLGIILFCSFKIVWSLRRRQQLARQARMK-KATRFIMVVAIVFITCYLP-SVSARL 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
                  Illinois
                                                      E: Borun
6300 Sears Tower,
                                                                                                                                                                             Gray, Patrick W.
Schweikart, Vicki L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                           Marshall, O'Toole, Gerstein, Murray &
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 336; DB 2;
Pred. No. 1.4e-21;
                                                      233 South Wacker Drive
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                                                                                                                                                    US-09-088-337B-44
                                                                                   Sequence 44, Application US/09088337B Patent No. 6348574 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 43,213
REFERENCE/DOCKET NUMBER: 27866/32059B
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
LENGTH: 339 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 07/977,452 FILING DATE: 17-NOV-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                     317 LKGPPPSFEGKTNESSLS 334
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARR: Patentin Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83 VLPTRLVYHFSGNHWPFGEIACRLTGFLFYLNMYASIYFLTCISADRFLAIVHP---VKS 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67 CLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNT 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
es 97; Conserv
Gray, Patrick W.
Schweikart, Vicki L.
TITLE OF INVENTION: No. 6348574el Seven Transmembrane Receptors
                                                                 APPLICANT: Godiska, Ronald
                                                                                                                                                                                                                                                                                                                                                                YFL-WTVPSSACDPSVHGAL--HITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLK 298
                                                                                                                                                                                                                                                                                                                                                                                                         AFTFPFITTVTCYLLIIRSL--RQGLRVEKRLKTKAVRMIAIVLAIFLVCFVPYHVNRSV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LKLRRPLYAHLACAFLWVVVAVAMAPLLVSPQTVQTNHTVVCLQLYREKASHHALVSLAV 199
                                                                                                                                                                                                                                                                                                                      YVLHYRSHGASCATQRILALANRITSCLTSLNGALDPIMYFFVAEKFRHALCNL-LCGKR 316
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(312) 474-0448
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Pred. No. 1.4e-21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 CRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMI 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6348574and, Greta E.
REGISTRATION NUMBER: 35,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/088,337B
FILING DATE: 01-Jun-1998
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM_PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 44:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: <Unknown> PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS
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                                        PKQPGHSKTQRPEEMPIS 316
                                                                                                                                                                          AFTFPFITTVTCYLLIIRSL--RQGLRVEKRLKTKAVRMIAIVLAIFLVCFVPYHVNRSV 257
                                                                                                                                                                                                EFFMPLGIILFCSFKIVWSLRRRQQLARQARMK-KATRFIMVVAIVFITCYLP-SVSARL 241
                                                                                                                                                                                                                                                          LKLRRPLYAHLACAFLWVVVAVAMAPLLVSPQTVQTNHTVVCLQLYREKASHHALVSLAV 199
                                                                                                                                                                                                                                                                                                                                                VLPTRLVYHFSGNHWPFGEIACRLTGFLFYLNMYASIYFLTCISADRFLAIVHP---VKS 139
                                                                                                                                                                                                                                                                                                                                                                                                                                     CGQETPLENMLFASFYLLDFILALVGNTLALWLFIRDHKSGTPANVFLMHLAVADLSCVL 82
LKGPPPSFEGKTNESSLS
                                                                                     YVLHYRSHGASCATQRILALANRITSCLTSLNGALDPIMYFFVAEKFRHALCNL-LCGKR 316
                                                                                                                           YFL-WTVPSSACDPSVHGAL--HITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLK 298
                                                                                                                                                                                                                                                                                                   ISTR--VAAGIVCT-LWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIMFQL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (312) 474-0448
TELEX: 25-3856
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
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30.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 336; DB 4;
Pred. No. 1.4e-21;
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RESULT 13
PCT-US93-11153-44
; Sequence 44, Applicat
; GENERAL INFORMATION:

Application PC/TUS9311153

Godiska, Ronald

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Best Local :
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 07
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Noland, Greta E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
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PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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317
                                 299 PKQPGHSKTQRPEEMPIS 316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Noland, Greta E. REGISTRATION NUMBER: 35,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 6300 :
CITY: Chicago
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                                                                                                          YFL-WTVPSSACDPSVHGAL--HITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLK 298
                                                                                                                                                                   EFFMPLGIILFCSFKIVWSLRRRQQLARQARMK-KATRFIMVVAIVFITCYLP-SVSARL 241
                                                                                                                                                                                                                                                              ISTR--VAAGIVCT-LWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIMFQL 183
LKGPPPSFEGKTNESSLS
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                                                                                                                                                                                                                                                                                                    VLPTRLVYHFSGNHWPFGEIACRLTGFLFYLNMYASIYFLTCISADRFLAIVHP---VKS 139
                                                                                                                                                                                                                                                                                                                                       CLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNT 126
                                                                                                                                                                                                                                                                                                                                                                           CGQETPLENMLFASFYLLDFILALVGNTLALWLFIRDHKSGTPANVFLMHLAVADLSCVL 82
                                                                                                                                                                                                                                                                                                                                                                                                              CRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMI 66
                                                                       YVLHYRSHGASCATQRILALANRITSCLTSLNGALDPIMYFFVAEKFRHALCNL-LCGKR 316
                                                                                                                                                AFTFPFITTVTCYLLIIRSL--RQGLRVEKRLKTKAVRMIAIVLAIFLVCFVPYHVNRSV 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                        l Similarity
97; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
GY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        339 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gray, Patrick W.
Schweikart, Vicki L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bicknell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Marshall, O'Toole, Gerstein, Murray &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                  18.1%; Score 336; DB 5; 30.5%; Pred. No. 1.4e-21; tive 54; Mismatches 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US 07/977,452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCT/US93/11153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31794
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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9

PCT-US95-07180-2 RESULT 14

Sequence 2,

Application PC/TUS9507180

US-08-467-948A-30; Sequence 30, Application US/08467948A; Patent No. 598164; GENERAL INFORMATION:
APPLICANT: LI, YI

밁

δÃ Дb

RESULT 15

QΥ

рь Qy Вb δÃ 뫄 Ωy В δÃ

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PCT-US95-07180-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: LI, YI
APPLICANT: GOCAYNE, JEANINE D
APPLICANT: RUBEN, STEVEN M
TITLE OF INVENTION: G-PROTEIN RECEPTOR HIBEB69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION: NAME: MULLINS, J.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                      242
                                                                                                                                                                                                                                            140
317 LKGPPPSFEGKTNESSLS
                                     299 PKQPGHSKTQRPEEMPIS 316
                                                                              258
                                                                                                                                                             200
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                                                                                                                                                                                                                                                                                 127
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                                                                                                                                                                                                                                                                                                                   83 VLPTRLVYHFSGNHWPFGEIACRLTGFLFYLNMYASIYFLTCISADRFLAIVHP---VKS 139
                                                                                                                                                                                                                                                                                                                                                                                                   23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                        67 CLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: MULLINS, J.G.
REGISTRATION NUMBER: 30,073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 06-JU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity es 97; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 07068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                     7 CRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMI 66
                                                                                                                  YFL-WTVPSSACDPSVHGAL--HITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLK 298
                                                                                                                                                                                EFFMPLGIILFCSFKIVWSLRRRQQLARQARMK-KATRFIMVVAIVFITCYLP-SVSARL
                                                                            YVLHYRSHGASCATQRILALANRITSCLTSLNGALDPIMYFFVAEKFRHALCNL-LCGKR 316
                                                                                                                                                         AFTFPFITTVTCYLLIIRSL--RQGLRVEKRLKTKAVRMIAIVLAIFLVCFVPYHVNRSV
                                                                                                                                                                                                                                      LKLRRPLYAHLACAFLWVVVAVAMAPLLVSPQTVQTNHTVVCLQLYREKASHHALVSLAV
                                                                                                                                                                                                                                                                               ISTR--VAAGIVCT-LWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIMFQL 183
                                                                                                                                                                                                                                                                                                                                                                                               CGQETPLENMLFASFYLLDFILALVGNTLALWLFIRDHKSGTPANVFLMHLAVADLSCVL 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-JUNE-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54; Mismatches 153;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 336; DB 5;
Pred. No. 1.4e-21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 339;
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Search completed: March 26, 2003, 19:39:49
Job time : 31 secs
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MEDIUM TYPE: FLOPPY DISK
COMPUTER: IEM PC COMPATIBLE
COMPUTER: IEM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,948A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04079
FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.

BEGIGFREATION NUMBER: 26.666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
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TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
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APPLICANT: BULT, CARCL J.
APPLICANT: SUTTON III, GRANGER G.
APPLICANT: ROSEN, CRRIG A.
TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein
TITLE OF INVENTION: Coupled Receptor GPR2
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                       196 VTCSTMVLRTLNKPLTLSRNKLSKKKVLKMIFVHLVIFCFCFVPYNITLILYSLMRTQTW 255
                                                                                                                                                                                                                                                                                                                                                                                                                           193 LFCSFKIVWSLRRRQQLAR-QARMKKATRFIMVVAIVFITCYLP-SVSARLYFLW---TV 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      139 VLAGSTPASFFQSTNRQNNTEQRTCFENF---PESTWKTYLSRIVIFIEIVGFFIPLILN 195
                                                                                                                                                                                        256 INCSVVTAVRTMYPVTLCIAVSNCCFDPIVYYFTSDTNSELDKKQQV 302
                                                                                                                                                                                                                                                                                  248 PSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKI 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            143 VILGTV---YLLLENHLCVQETAVSCESFIMESANGWHDIMFQL------EFFMPLGII 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1100 NEW CITY: WASHINGTON STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        y Match 17.7%; Score 328.5; DB 2; Local Similarity 30.0%; Pred. No. 5.4e-21; nes 86; Conservative 58; Mismatches 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80 GDVLCKISVTLFYTNMYGSILFLTCISVDRFLAIVHPFRS-KTLRTKRNARIVCVAVWIT 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84 GDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVAAGIVC-TLWAL 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 VAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFILMICLPFRTDYYLRRRHWAF 83 : || | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
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NI, JIAN
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Published_Applications_AA:*

1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
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Gapop 10.0 , Gapext 0.5
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1853
1 MYNGSCCRIEGDTISQVMPP.....ANSFQSQSDGQWDPHIVEWH 346
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

19.8 346 9 19.8 346 10 19.8 346 10 19.8 346 10 19.6 362 9 19.6 362 9 19.6 373 9 19.3 373 9 19.1 373 9	Result No. 1 2 3 3 4 4 7 7 7 10	Score 1853 1853 1853 1849 1739 880.5 880.5 880.5 366.5	Query Match 100.0 100.0 99.8 93.8 47.5 47.5 24.5 24.1 19.8	Query Match Length DB Match Le	100 100 100 100 100 100 100	US-09-862-274-2 US-09-962-274-2 US-10-094-417-8 US-10-092-135-2 US-10-092-135-8 US-09-944-807-21 US-09-826-508-40 US-10-092-135-9 US-10-092-135-9 US-10-109-549-2 US-09-886-791-2	Sequence 2, Sequence 2, Sequence 2, Sequence 8, Sequence 8, Sequence 8, Sequence 9, Sequence 9, Sequence 2, Sequence 3, Sequen
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HHAVNT	DFLLMIC	1 MYNGSCCI	Match Local Simi les 346;	T 1 -862-274-2 uence 2, App ent No. US20 ERAL INFORMA PLICANT: ELS PLICANT: ELS PLICANT: GA PLICANT: IG TLE OF INVEN TLE OF STOLIC TRENT FILING TOR FILING D TOR APPLICAT TOR APPLICAT TOR FILING D TOR FELING D TOR FILING D TOR FELING D TOR FELING D TOR FELING D TOR FELING D TOR APPLICAT TOR TELING D TOR		292.5	294	298.5 298	_)	302	305	-	309.5	320	328.5		336 336	343
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GIVCTLWALVI GIVCTLWALVI	YLRRR 	SQVMP MVQS	100 100 rative	DD US/ D22A1 Y NA HANAN SMANN JANE M OTHER OTHER J703-1 1000-0 1000-1 1000-1 1000-1 1000-1 VWind		365	372	418 428	428	391	337	372	337	363	344	309	367	339 339	299
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LGTVYLLLENHLCVQETAVSCESF	LPERTDYYLRRRHWAFGDIPCRVGLETLAMNRAGSIVFLTVV 	SQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA	; Score 1853; DB 10; Leng ; Pred. No. 1.6e-169; 0; Mismatches 0; Indel	NG OF A CHEMOKINE LIK 62,274 ,675 9.1 on 3.0	ALIGNMENTS	US-09-992-331-13 US-10-109-533A-2	US-10-112-599A-4	US-09-992-331-17	US-09-823-114-9 US-09-992-331-15	US-10-039-645-82	US-10-167-192-3 US-10-167-192-3	US-10-167-192-5	US-09-828-478-5	US-10-116-252-10 US-09-992-331-14 US-09-990-940-20	US-10-024-494-8 US-10-270-587-3	US-10-024-494-30 US-09-768-877-20	US-09-788-133-2 US-09-828-478-6	US-09-828-478-4 US-09-848-889-12	US-10-270-144-4
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                                                              GENERAL INFORMATION:
                                                                               Sequence 8, Application US/10094417 Publication No. US20030045685A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 2
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Best Local Similarity
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CURRENT FILING DATE: 2001-08-29
PRIOR APPLICATION NUMBER: US 60/228,409
PRIOR FILING DATE: 2000-08-29
NUMBER OF SEQ ID NOS: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Gimeno, Ruth
APPLICANT: White, David
TITLE OF INVENTION: 87242, a Human G-Protein Coupled
TITLE OF INVENTION: Receptor Family Member and Uses Therefor
FILE REFERENCE: MPI2000-368P1R
APPLICANT: Tian, Hui
APPLICANT: Zhao, Jia
APPLICANT: Chen, Jia
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TYPE: PRT
ORGANISM: human
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Zhao, Jiagang
Chen, Jin-Long
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APPLICANT: Cutler, Gene
APPLICANT: Tularik Inc.
TULArik Inc.
TITLE OF INVENTION: NO. US20030045685A1el Receptors
FILE REFERENCE: 018781-008110US
CURRENT APPLICATION NUMBER: US/10/094,417
CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: US 09/802,803
PRIOR APPLICATION NUMBER: US 09/802,803
PRIOR FILING DATE: 2001-03-09
PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 43
NUMBER OF SEQ ID NOS: 43
                                             ; ORGANISM: homo US-10-092-135-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-092-135-2
                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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LENGTH: 346
                                                                                                                                 SEQ ID NO 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                     APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLECTIDE ENCODING A NOVEL HUMAN G-PROTEIN COUPLED RECEPT
TITLE OF INVENTION: HGRBMY27
FILE REFERENCE: D0134.NP
CURRENT APPLICATION NUMBER: US/10/092,135
CURRENT FILING DATE: 2002-03-06
PRIOR APPLICATION NUMBER: US 60/273,808
PRIOR APPLICATION NUMBER: US 60/273,808
PRIOR FILING DATE: 2001-03-07
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                                                                                                                                                      SOFTWARE: PatentIn version 3.0
                                                                                                                                                                          NUMBER OF SEQ ID NOS:
                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/278,983 PRIOR FILING DATE: 2001-03-27
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                                                                                        TYPE: PRT
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                                                                                                          LENGTH:
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Pred. No. 3.9e-169;
  Score 1739;
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Length 342;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn version 3.0 SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
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PRIOR FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 60/278,983
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 75
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CURRENT APPLICATION NUMBER: US/10/092,135
CURRENT FILING DATE: 2002-03-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 387
TYPE: PRT
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                     245 WTVPSSA---CD--PSVHGALHITLSETYMNSMLDPLVYYESSPSEPKFYNKLKICSLKP 299
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                                                                        FLLPLGIILFCSARIIWSLRQR-QMDRHAKIKRAITFIMVVAIVFVICFLPSVVVRIRIF 255
                                                                                                                                                            NKISNWTAAIISCLLWGITVGLTVHLLKKKLLIQNGPANVCISFSICHTFRWHEAMFLLE 196
                                                                                                                                                                                                                                                       IICLPFVMDYYVRRSDWNFGDIPCRLVLFMFAMNRQGSIIFLTVVAVDRYFRVVHPHHAL 136
                                                                                                                                                                                                                                                                                                                                                NCCVFRDDFIAKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWKSSRIFLFNLAVADFLL 76
                                                                                                                                                                                                                                                                                                                                                                                              SCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLL 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               47.5%; Score 880.5; DB 9 52.2%; Pred. No. 2.2e-76;
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                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Nabil Elshourbagy
APPLICANT: Lisa Vawter
                                                                                                                                                                                                                                                     Sequence 40, Application US/09826508 Patent No. US20010025099A1
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SEQ ID NO 40
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Best Local :
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                CURRENT APPLICATION NUMBER: US/09/826,508
CURRENT FILLING DATE: 2001-04-05
NUMBER OF SEO ID NOS: 40
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                  TITLE OF INVENTION: G Protein-Coupled Receptor Polypeptides TITLE OF INVENTION: and Polynucleotides FILE REFERENCE: GP-70744USB
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CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: UK 0021484.1
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TITLE OF INVENTION: Method for identifying substances which positively
TITLE OF INVENTION: influence inflammatory conditions of chronic
TITLE OF INVENTION: inflammatory airway diseases
FILE REFERENCE: 082_00n
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                                                                                                                                                                                                                                                                                                                                                                                                                                     KQPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDP 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPSFPNFFSTLINRCLQR 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSARLYFL 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIMFQLE 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCCVFRDDFIAKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWKSSRIFLFNLAVADFLL 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NKISNWTAAIISCLLWGITVGLTVHLLKKKLLIQNGPANVCISFSICHTFRWHEAMFLLE 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IICLPFVMDYYVRRSDWNFGDIPCRLVLFMFAMNRQGSIIFLTVVAVDRYFRVVHPHHAL 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KMTGEPDNNRSTSVELTGDPNKT-RGAPEALMANSGEPWSP 355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47.5%; Score 880.5; DB 1 52.2%; Pred. No. 2.2e-76;
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Gaps 64

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241 -- LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKL 292

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US-09-826-508-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-092-135-9
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                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 115;
                                                                                                                                                                                                                                                                                                                                                                  Matches 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/092,135
CURRENT FILING DATE: 2002-03-06
PRIOR APPLICATION NUMBER: US 60/273,808
PRIOR FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 60/278,983
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NUMBER OF SEQ ID NOS: 75
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR,
TITLE OF INVENTION: HGPREMY27
FILE REFERENCE: D0134.NP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: HOMO SAPIENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124 VNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQE-TAVSCESFIM----ESANGWHD 178
  183 CLQFVLPFGLIVFCNAGIIRALQKRLREPEKQPKLQRAQALVTLVVVLFALCFLPCFLAR
                                              182 QLEFFMPLGIILFCSFKIVWSLRRR-QQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              141 LISNLPLRYDYYLLHETWRFGAAACKYNLFMLSTNRTASVVFLTAIALNRYLKYVQPHHV 200
                                                                                                                                                                                     66
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                                                                                                                                                                                                                                                                                                                                                                                     Match 24.2%; Score 448.5; DB 9 Local Similarity 34.0%; Pred. No. 3.8e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 LMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81 GPCHPTSSSLVSAFLAPILALEFVLGLVGNSLALFIFCIHTRPWTSNTVFLVSLVAADFL 140
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                                                                                                                                                                                                                                                                                                                   7 CRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMI 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 GSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGECFHMKTWKPSTVYLFNLAVADFL 63
                                                                                                                                    ISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANG-----WHDIMF 181
                                                                                                                                                                                                                             CLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --SARLYFLWTVPSSA---CDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSF 285
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                                                                                             LSPQAALGVSGLVWLLMVALTCPGLLISE--AAQNSTRCHSF-YSRADGSFSIIWQEALS
                                                                                                                                                                                                                                                                         CSAPSTVVATAVGVLLGLECGLGLLGNAVALWTFLFRVRVWKPYAVYLLNLALADLLLAA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALYLLEFFLPLALILFAIVSIGLTIRNR-GLGGQAGPQRAMRVLAMVVAVYTICFLPSII 313
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                                                                                                                                                                                   CLPFLAAFYLSLQAWHLGRVGCWALRFLLDLSRSVGMAFLAAVALDRYLRVVHPRLKVNL 125
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                                                                                                                                                                                                                                                                                                                                                                  62; Mismatches 121;
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US-09-826-791-2

GENERAL INFORMATION: APPLICANT: Pfizer Inc

PRIOR APPLICATION NUMBER: 0008504.3
PRIOR FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: 60/198,367
PRIOR FILING DATE: 2000-04-19

CURRENT APPLICATION NUMBER: US/09/826,791 CURRENT FILING DATE: 2001-04-05

TITLE OF INVENTION: NO. US20010039037A1el Polypeptide FILE REFERENCE: PC10914ADAM

Sequence 2, Application US/09826791 Patent No. US20010039037A1

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RESULT 10
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
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APPLICANT: Brennan, Thomas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Matthews, William APPLICANT: MOOTE, Mark TITLE OF INVENTION: TRANSCENIC MICE CONTAINING TITLE OF INVENTION: DISRUPTIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/109,549
CURRENT FILING DATE: 2002-07-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: R-180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Mus musculus
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                                                                                                                                                                                                                                                                                       182 QLEFFMPLGIILFCSFKIVWSLRRR-QQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240
                                                                                                                                                                                                                                                                                                                                                             126 LSLRAAWGISSLIWLLMVVLTPQNLL---TCRTTQNSTECPSFYPTGGTKAIATCQEVLF 182
                                                                                                                   299 PKQPGHSKTQRPEEMPISNL 318
                                                                                                                                                                 243 VLVHIFQEFKSCSVQQAIMRASDIAGSLTCLHSTLSPAIYCFSNPAFTHSYRKV-LKSLR 301
                                                                                                                                                                                                                                                              183 FLQVLLPFGLISFCNSGLIRTLQKRLSESDKQPTIRRARVLVAIMLLLFGLCFLPSVLTR 242
                                                                                                                                                                                                                                                                                                                                                                                                           127 ISTRVAAGIVCTLWALVILGTVYLLLENHLC-VQETAVSCESFI----MESANGWHDIMF 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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                                                                                                                                                                                                              --LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLK 298
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                                                                      -RKAAESPSDNL 314
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Pred. No. 5.9e-35;
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; LENGTH: 346
; TYPE: PRT
; ORGANISM: HOMO S
US-09-828-478-2
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TITLE OF INVENTION: Regulation of Human CysLT2-Like GPC
TITLE OF INVENTION: PROTEIN
FILE REFERENCE: 04974,00458
CURRENT APPLICATION NUMBER: US/09/828,478
CURRENT FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: 60/195,196
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: 60/254,876
PRIOR APPLICATION NUMBER: 60/254,876
PRIOR FILING DATE: 2000-12-13
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                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/09828478 Patent No. US20020155528A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver.
SEQ ID NO 2
LENGTH: 330
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TYPE: PRT
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                                                                          ADFILMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVH 119
                                                                                                                 NSRNCTIE-NFKREFFPIVYLIIFFWGVLGNGLSIYVF---LQPYKKSTSVNVFMLNLAI 82
                                      SDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLAMVH 142
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LENGTH: 346
TYPE: PRT
ORGANISM: Homo sapiens
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CURRENT APPLICATION NUMBER: US/09/826,791
CURRENT FILING DATE: 2001-04-05
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NUMBER OF SEQ ID NOS: 6
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Local Similarity 29.9%;
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                               CSLKPKQPGHSKTQ 308
SALRKGHPQKAKTK 331
                                                                                                                                       NYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIIITLIIFFLCFL
                                                                                                   PSVSARLYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKI
                                                                   PYHTLRTVHLTTWKVGLCKDRLHKALVITLALAAANACFNPLLYYFAGENFK---DRLK-
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Pred. No. 3e-27;
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RESULT 13 US-09-866-230-7

Sequence 7, Application US/09866230 Patent No. US20020150901A1

GENERAL INFORMATION:

APPLICANT: Murphy,

Andrew, et al

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                                                                                                                                                                                                                                ; ORGANISM: Homo sapiens US-09-866-230-9
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APPLICANT: MUIPBY, Andrew, et al.
APPLICANT: MUIPBY, Andrew, et al.
TITLE OF INVENTION: No. US20020150901A1el Nucleic Acids, Polypeptides, Methods of Mal
FILE REFERENCE: REG 771A
CURRENT APPLICATION NUMBER: US/09/866,230
CURRENT FILING DATE: 2001-05-25
CURRENT FILING DATE: 2001-05-25
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Best Local
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Best Local Similarity
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FILE REFERENCE: REG 771A
CURRENT APPLICATION NUMBER: US/09/866,230
CURRENT FILING DATE: 2001-05-25
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PRIOR FILING DATE: 2000-05-26
NUMBER OF SEQ ID NOS: 9
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ORGANISM: Homo sapiens
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NSRNCTIE-NFKREFFPIVYLIIFFWGVLGNGLSIYVF---LQPYKKSTSVNVFMLNLAI 82
                                                                                          NGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPST---VYLFNLAV 59
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                                                              NSRNCTIE-NFKREFFPIVYLIIFFWGVLGNGLSIYVF---LQPYKKSTSVNVFMLNLAI 82
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Pred. No. 3e-27;
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APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLECTIDE ENCODING A NOVEL HUMAN G-PROTEIN COUPLED RECEPT
TITLE OF INVENTION: HGPRBMY27
FILE REFERENCE: D0134.NP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/10092135 Publication No. US20030054374A1
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PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/092,135
CURRENT FILING DATE: 2002-03-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/273,808 PRIOR FILING DATE: 2001-03-07
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TYPE: PRT
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327 ATRKSSRRSEP--NVQSKSEEMTLNIL
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                                                                                                                                     ----SVSARLYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNK 291
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300 KQPGHSKTQRP 	Qy 125 NTISTRVAAGIVCTUMALVILGTVYLLLENHICVOETAVSCESFINESANGHDINGLE	5 SCCRIE 17 NCCVER 65 MICLPE 17 IICLPE	RESULT 1 169202 G protein-coupled receptor HM74 - human C;Species: Homo sapiens (man) C;Species: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change C;Accession: 169202 R;Nomura, H.; Nielsen, B.W.; Matsushima, K. Int. Immunol. 5, 1239-1249, 1993 A;Title: Molecular cloning of cDNAs encoding a LD78 receptor an A;Reference number: 154751; MUID:94092629; PMID:7505609 A;Recession: 169202 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-387 (RES> A;Cross-references: GB:D10923; NID:g219866; PIDN:BAA01721.1; PI C;Genetics: A;Gene: HM74 C;Superfamily: G protein-coupled receptor 4 C;Superfamily: G protein-coupled receptor 4 Ouery Match Guery Match Matches 178; Conservative 49; Mismatches 107; Indels	30 296 16.0 359 2 A48857 31 296 16.0 375 2 A54946 32 295 15.9 384 2 JC4629 33 295 15.8 361 2 JC5483 35 292 15.8 361 2 JC5483 36 291.5 15.7 359 2 S44425 37 291.5 15.7 359 2 JC2134 38 290 15.7 372 2 S34592 39 289 15.6 359 2 JC21104 40 288 15.5 359 2 JC21104 41 288 15.5 359 2 JC2177 42 287.5 15.5 372 2 B48227 42 287.5 15.5 372 2 B48227 44 286.5 15.5 371 2 JC5796 44 286.5 15.5 371 2 JC5796 45 286.5 15.5 359 2 JH0661 46 286.5 15.5 359 2 JH0661 47 287.5 15.5 371 2 JC7677
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RESULT 2 333733 G protein-coupled receptor - chicken C; Species: Gallus gallus (chicken)

R;Webb,

;Accession: S33733

06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 24-Sep-1999

T.E.

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C;Genetics:
A;Gene: bovp2y
A;Gene: bovp2y
C;Superfamily: ATP receptor P2u
C;Keywords: glycoprotein; phosphoprotein; receptor; tra
C;Keywords: transmembrane #status predicted <TM1>
F;52-77/Domain: transmembrane #status predicted <TM2>
F;88-111/Domain: transmembrane #status predicted <TM2>
                                                                                                                                                                                                                F;124-150/Domain: transmembrane #status predicted <TM3>
F;171-191/Domain: transmembrane #status predicted <TM4>
F;271-237/Domain: transmembrane #status predicted <TM5>
F;261-282/Domain: transmembrane #status predicted <TM6>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochem. Biophys. Res. Commun. 212, 648-656, 1995
A;Tittle: Cloning and characterisation of a bovine P2Y receptor
A;Reference number: JC4162; MUID:95352058; PMID:7626079
A;Accession: JC4162
A;Molecule type: mRNA
A;Residues: 1-373 <HEN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Bos primigenius taurus (cattle)
C;Date: 12-Oct-1995 #sequence_revision 10-Nov-1995 #text_change 24-Sep-1999
C;Cate: 12-Oct-1995 #sequence_revision 10-Nov-1995 #sequence
                                                                                                F;258/Binding
                                                                                                                                                                              F:305-328/Domain: transmembrane #status predicted <TM7>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:X87628; NID:g1032484; PIDN:CAA60958.1; PID:g1032485 A;Experimental source: aortic endothelial cell
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A; Residues: 1-362 <WEB>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEBS Lett.
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              Query Match
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                                                                                                                                                 27,113,197/Binding site:
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324, 219-225, 1993
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         19.6%;
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                                                                                                                                       carbohydrate (Asn)
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    Score 362.5;
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Length 373
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A; Map position: 3pter-3qter
C; Superfamily: ATP receptor P2u
C; Superfamily: ATP receptor P2u
C; Keywords: G protein-coupled receptor; glycoprotein; F; 52-77/Domain: transmembrane #status predicted < TMI)
                                                                                                                                                                                                                                                                                                    A; Dialus, Free mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-137,139-373 <LEO>
A; Cross-references: EMBL: Z49205; NID: g798835; PIDN: CAA89066.1; PID: g798836
A; Cross-references: EMBL: Z49205; NID: g798835; PIDN: CAA89066.1; PID: g798836
A; Cross-references: EMBL: Z49205; NID: g798835; PIDN: CAA89066.1; PID: g798836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Ayyanathan, K.; Webbs, T.E.; Sandhu, A.K.; Athwal, R.S.; Barnard, E.A.; K Biochem. Biophys. Res. Commun. 218, 783-788, 1996
A;Title: Cloning and chromosomal localization of the human P2Y1 purinocepto. A;Reference number: JC4615; MUID:96158962; PMID:8579591
A;Molocalization JC4615
F;124-152/Domain: transmembrane #status predicted <TM3>F;171-191/Domain: transmembrane #status predicted <TM4>F;214-237/Domain: transmembrane #status predicted <TM5>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        G protein-coupled receptor P2Y1 - human

N;Alternate names: P2Y1 purinergic receptor; P2Y1 purinoceptor

C;Species: Homo sapiens (man)

C;Date: 10-May-1996 #sequence_revision 16-Aug-1996 #text_change 17-Nov-2000

C;Accession: JC4737; JC4615; S54253

C;Accession: JC4737; JC4615; Pirotton, S; Samson, M.; Parmentier, M.; Boeynaems, R;Janssens, R.; Communi, D.; Pirotton, S; Samson, M.; Parmentier, M.; Boeynaems, Biochem. Biochys. Res. Commun. 221, 588-593, 1996

A;Title: Cloning and tissue distribution of the human P2Y1 receptor.

A;Reference number: JC4737; MUID:96205320; PMID:8630005
                                                                                                                                                                                                                                                         A; Cross-references: GDB:677125;
                                                                                                                                                                                                                                                                                             A; Gene: p2Y1; GDB: P2RY1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Leon, C.; Vial, C.; Cazenave, J.; Gachet, C. submitted to the EMEL Data Library, May 1995 A;Description: Cloning of a human putative P2Y receptor. A;Reference number: S54253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:U42029; NID:g1147730; A;Experimental source: erythro leukemia cells R;Leon, C.; Vial, C.; Cazenave, J.; Gachet, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: S54253
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A; Residues: 1-373 <AYY>
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A; Residues: 1-373 <JAN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKIKICSLKPK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               174 LVWLIVVVGISPILFYSGTGIRKNKTITCYDTTSDEYLRSYFIYSM-----CTTVAMFCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          138 TLWALVILGTVYLLLENHLCVQET-AVSC-----ESFIMESANGWHDIMFQLEFFM 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         114 KTDWIFGDAMCKLQRFIFHVNLYGSILFLTCISAHRYSGVVYPLKSLGRLKKKNAVYISV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54 LPAVYILVFIIGELGNSVAIWMEVFHMKPWSGISVYMFNLALADELYVLTLPALIFYYFN 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18 MPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMICLPFRTDYYLR 77
                                                                                            /Domain: transmembrane #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --ATRKASRRSEANLQSKSEDMTLNILSEFKQNGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LDF-QTPEMCAFNDRVYATYQVTRGLASLNSCVDPILYFLAGDTFRRRLSR------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVAAGIVC 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NID: g1147730; PIDN: AAA97872.1; PID: g1147731
                                                                                                                                                                                                                                                             OMIM: 601167
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                                                                                                                                                          glycoprotein; phosphoprotein; transmembrane
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                                                                                                  <TM2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Barnard, E.A.; Kunapuli,
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                                                                                                                                                                                                                                                                                                                                                  receptors.
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F;261-282/Domain: transmembrane #status predicted <TM6>
F;305-328/Domain: transmembrane #status predicted <TM7>
F;305-328/Domain: transmembrane #status predicted <TM7>
F;11,27,113,197/Binding site: carbohydrate (Asn) (covalent) #status predicted F;258,336/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predict F;330,339/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predict F;343/Binding site: phosphate (Ser) (covalent) (by protein kinase C and calmodulin-dependent)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R.Janssens, R.; Boeynaems, J.M.; Godart, M.; Communi, D. Biochem. Biophys. Res. Commun. 236, 106-112, 1997 A;Title: Cloning of a human heptahelical receptor closely A; Reference number: JC5549; MUID:97366605; PMID:9233435 A; Accession: JC5549
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;MoLecule type: DNA A;Residues: 1-370 <JAN> A;Residues: 1-370 <JAN> A;Cross-references: DDBJ:AF005419; NID:g2240034; PIDN:AAB66322.1; C;Superfamily: ATP receptor P2u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Homo sapiens (man)
C;Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 24-Sep-1999
C;Accession: JC5549
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-- Tocal Similarity
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                                                                                                                                                                                                                                            107
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                                                                                                                                                                                                                                                                                                                                                                                      24 VAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMICLPFRTDYYLRRRHWAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVAAGIVC 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LPAVYILVFIIGFLGNSVAIWMFVFHMKPWSGISVYMFNLALADFLYVLTLPALIFYYFN 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LVWLIVVVAISPILFYSGTGVRKNKTITCYDTTSDEYLRSYFIYSM-----CTTVAMFCV
                                                                                                                                                                                         VILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIMFQLE----FFMPLGIILFC
                                                                                                                                                                                                                                                                                                                                         VVFILGLITNSVSLFVFCFRMKMRSETAIFITNLAVSDLLFVCTLPFKI-FYNFNRHWPF 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PLVLILGCYGLIVRALIYK-DLDNSPLRRKSIYLVIIVLTVFAVSYIPFHVMKTMNLRAR
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                                                  SSVVLRTLRKPATLSQIGTNKKKVLKMITVHMAVFVVCFVPYNS--VLFLYALVRSQAIT
                                                                                               SFKIVWSLRRRQQLAR-QARMKKATRFIMVVAIVFITCYLPSVSARLYFLWTVPSSAC--
                                                                                                                                               VLSGGISASLFSTTNVNNATTTC--FEGLSKRVWKTYLSKITIFIEVVGFIIPLILNVSC
                                                                                                                                                                                                                                            GDTLCKISGTAFLTNIYGSMLFLTCISVDRFLAIVYPFRS-RTIRTRRNSAIVCAGVWIL
                                                                                                                                                                                                                                                                                         GDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVAAGIVCT-LWAL 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LDF-QTPAMCAFNDRVYATYQVTRGLASLNSCVDPILYFLAGDTFRR----RLSRATRKAS 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93;
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  -DPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPK-FYNKLKICSLKPKQPGHSKT
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31.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 343.5; DB 2
Pred. No. 3.8e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 354; DB 2; Pred. No. 4.1e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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J. Immunol. 151, 628-636, 1993
A;Title: Identification of a G protein coupled receptor A;Reference number: I50241; MUID:93329058; PMID:8393036 A;Accession: I50241
A;Status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:L06109; NID:g304383; PIDN:AAB06587.1; R;Webb, T.E.; Kaplan, M.G.; Barnard, E.A.
Biochem. Biophys. Res. Commun. 219, 105-110, 1996
A;Title: Identification of 6H1 as a P2Y purinoceptor: P2Y5.
A;Reference number: JC4618; MUID:96190677; PMID:8619790
A;Accession: JC4618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change
C;Accession: I50241; JC4618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;227-248/Domain: transmembrane *status predicted <TM6> F;269-292/Domain: transmembrane *status predicted <TM7>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: p2Y5
C;Superfamily: ATP receptor P2u
C;Superfamily: ATP receptor P2u
C;Keywords: G protein-coupled receptor; transmembrane protein
C;Keywords: G protein-coupled receptor; transmembrane protein
F;15-40/Domain: transmembrane #status predicted <TM2>
F;51-74/Domain: transmembrane #status predicted <TM2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Experimental source: T-cells C; Comment: This receptor plays a role in T-cell activation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: mRNA
A;Residues: 1-308 <WEB>
A;Cross-references: GB:L06109; NID:g304383; PIDN:AAB06587.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Residues: 1-308 < KAP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               G protein-coupled receptor 6H1 - ch N; Alternate names: purinoceptor 6H1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    I50241
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F;177-201/Domain: transmembrane #status predicted <TM5>
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  258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
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                                                                                                                                                                                                                                                                                                                                                      GDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVAAGIVC-TLWAL 142
                                                                                                                                                                                                                                                                                                                                                                                                     MVFVLGLIANCVAIYIFTETLKVRNETTTYMLNLAISDLLFVFTLPFRI-YYFVVRNWPF 81
INCSYVTAVRTMYPVTLCIAVSNCCFDPIVYYFTSDTNSE-
                                                                                                                                   LFCSFKIVWSLRRRQQLAR-QARMKKATRFIMVVAIVFITCYLP-SVSARLYFLW---TV
                                                                                                                                                                                                                                                  VILGTV---YLLLENHLCVQETAVSCESFIMESANGWHDIMFQL-----EFFMPLGII 192
                                                                                                                                                                                                                                                                                                    GDVLCKISVTLFYTNMYGSILFLTCISVDRFLAIVHPFRS-KTLRTKRNARIVCVAVWIT 140
                                               PSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPKQPGHSKT 307
                                                                                                 VTCSTMVLRTLNKPLTLSRNKLSKKKVLKMIFVHLVIFCFCFVPYNITLILYSLMRTQTW
                                                                                                                                                                                                     VLAGSTPASFFQSTNRQNNTEQRTCFENF --- PESTWKTYLSRIVIFIEIVGFFIPLILN 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 339; DB 2;
Pred. No. 8.2e-24;
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  LDKKQQVHQNT 308
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                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Expression cloning of an ATP receptor from mouse neuroblastoma A;Reference number: A47556; MUID:93281707; PMID:7685114
A;Accession: A47556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATP receptor P2u - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-Sep-1999
                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-373 < LUS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R; Lustig, K.D.; Shiau, A.K.; Brake, A.J.; Julius, D. Proc. Natl. Acad. Sci. U.S.A. 90, 5113-5117, 1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Description: The human p
A; Reference number: Z16705
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Residues: 1-344 <BOH>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDB
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                                                                                                                                                                                                                                  Query Match
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82 YAASLPLLVYYYARGDHWPFSTVLCKLVRFLFYTNLYCSILFLTCISVHRCLGVLRPLHS
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                                                                                                                                                                                                              POCST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 VAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMICLPFRTDYYLRRRHWAF 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
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                                           LMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHA 123
                                                                                                                                   GSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFL
                                                                                      GYKCRFNEDFKYVLLPVSYGVVCVLGLCLNVVALYIFLCRLKTWNASTTYMFHLAVSDSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCSVVAAVRTMYPITLCIAVSNCCFDPIVYYFTSDT---IQNSIKM 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VILGT--VYLLLENHLCVQETAVSCESFIMESANGWHDIMFQL-----EFFMPLGIIL 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FCSFKIVWSLRRRQQLARQARMK-KATRFIMVVAIVFITCYLP-SVSARLYFL---WTVP 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VIGGSAPAVFVQSTHSQGNNASEACFENFPEAT--WKTYLSRIVIFIEIVGFFIPLILNV 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVAAGIVCT-LWAL 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKI 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCSSMVLKTLTKPVTLSRSKINKTKVLKMIFVHLIIFCFCFVPYNINLILYSLVRTQTFV 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GDLLCKISVMLFYTNMYGSILFLTCISVDRFLAIVYPFKS-KTLRTKRNAKIVCTGVWLT 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88;
                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17.5%; Score 324; 30.8%; Pred. No. 2
                                                                                                                                                                                   44; Mismatches 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56;
                                                                                                                                                                                                       Score 320; DB 2;
Pred. No. 5.9e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NID:g2232068; PID:g2232069
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                                                                                                                                                                                                                         Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    thrombin receptor - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C;Accession: I51667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δÃ
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A; Residues: 1-420 <GER>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Title: Thrombin receptor's specificity for agonist peptide is determined by its ext A; Reference number: I51667; MUID:94195429; PMID:8145852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Db
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 368,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R; Gerszten, R.E.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      100
                                      295 CSLKPKQPGHSKTQ 308
                                                                                                                                                                                                                                                                                            134 GIVCT-LWALVILGTVYLLL--ENHLCVQETAVSCESFI-MESANGWHDIMFQ----LEF 185
                                                                                                                                                                                                                                                                                                                                                160
382 CCRKVSEPGSSTGQ
                                                                                                                                                                                                                                                                                                                                                                                74 YYLRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVAA 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14 ISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMICLPFRTD 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            312 RLVRFARDAK----PPTEPTPSPQAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  284 SFPKFYNKLKICSLKPKQPGHSKTQR 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124 VNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCES------FIMESAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                   QEANEFLYFAYIL -- SACVGSV--
                                                                                                                       PSVSARLYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKI
                                                                                                                                                                  FVPFIITTICYIGIIRSL-SSSSIENSCKKTRALFLAVVVLCVFIICFGPTNVLFLTHYL
                                                                                                                                                                                                             FMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITC----
                                                                                                                                                                                                                                                      YMACSFIWLISIASTIPLLVTEQTQKIPRLDITTCHDVLDLKDLKDFYIYYFSSFCLLFF
                                                                                                                                                                                                                                                                                                                                       YHLSGNDWLFGPGMCRIVTAIFYCNMYCSVLLIASISVDRFLAVVYPMHSLSW-RTMSRA 218
                                                                                                                                                                                                                                                                                                                                                                                                                             LTKEVPSLYTVVFIVGLPLNLLAIIIFLFKMKVRKPAVVYMLNLAIADVFFVSVLPFKIA 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AVFALCFLPFHVTRTLYYSFRSLDLSCHTLNAINMAYKITRPLASANSCLDPVLYFLAGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IVFITCYLP-SVSARLYFLWTVPSSACDP--SVHGALHITLSFTYMNSMLDPLVYYFSSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----VMLGLLFAVPFSVILVC---YVLMARRLLKPAYGTTGGLPRAKR--KSVRTIALVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GWHDIMFQLEFFMPLGIILFCSFKIVWSLRRRQQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LRWGRARYARRVAAVVWVLVLACQAPVLYFVTTSVRGTRITCHDTSARELFSHFVAYSS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R.E.; Chen, J.; Ishii, M.; Ishii, K.; Nanevicz, 648-651, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 310.5; DB Pred. No. 5.1e-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   133;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37;
                                                                                                                                                                                                             -YL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                       294
                                                                                                                                                                  337
                                                                                                                                                                                                             234
                                                                                                                                                                                                                                                        278
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A; Title: Molecular cloning and expression of a pituitary somatostatin receptor with

R; O'Carroll, A.M.; Lolait, S.J.; Konig, M.; Mahan, L.C.

939-946,

1992

C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 24-Nov-1999 C;Accession: 157940; 157949; S39244

C; Species: Rattus norvegicus (Norway rat)

somatostatin receptor 5 - rat

N;Alternate names: somatotropin release-inhibiting factor

subtype 28 receptor

Mo]

Pharmacol. 42,

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R;O'Carroll, A.M.; Lolait, S.J.; Konig, M.; Mahan, L.C. Mol. Pharmacol. 44, 1278, 1993
A;Title: Molecular cloning and expression of a pituitary A;Reference number: 157949; MUID:94088493; PMID:8264565
A;Accession: 157949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:X74828; NID:g433911; PIDN:CAA52825.1; C;Genetics:
A;Gene: SSTR5
C;Superfamily: vertebrate rhodopsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Reference number: S39244
A; Accession: S39244
A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Experimental source: pituitary
R;Penetta, R.; Greenwood, M.; Patel, Y.C.
submitted to the EMBL Data Library, August 1993
A;Description: Correction of the nucleotide and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Reference number: 157940; MUID:93125499; PMID:136
A;Accession: 157940
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A; Residues: 1-391 <YAM>
A; Cross-references: GB: M81831; NID: g201058; C; Superfamily: vertebrate rhodopsin
                                               A;Status: nucleic acid sequence not shown A;Molecule type: DNA A;Residues: 1-391 <YAM>
                                                                                                                                                                            R;Yamada, Y.; Post, S.R.; Wang, K.; Tager, H.S.; Bell, G.I.; Seino, Proc. Natl. Acad. Sci. U.S.A. 89, 251-255, 1992
A;Title: Cloning and functional characterization of a family of hum
                                                                                                                                                                                                                                                                         somatostatin receptor 1 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 31-Dec-1993 #text_change 24-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Qy
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                                                                                                                            A; Reference number: A41795; MUID:92108031; PMID:1346068 A; Accession: C41795
                                                                                                                                                                                                                                 C; Accession: C41795
R; Yamada, Y.; Post,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 309-363 < PEN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:S67370; NID:g455947;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 341-363 < OCA2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   333 IEPRPDKSGRPQ----ATLPTRSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       193 LFCSFKIVWSLR----RRQQLARQARMK-KATRFIMVVAIVFITCYLPSVSARLYFL-WTV 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 VMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADELLMICLPFRTDYYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KQPGHSKTQRPEEMPISNLGRRSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLCYLLIVVKVKAAGMRVGSSRRRRSEPKVTRMVVVVVVLVFVGCWLPFFIVNIVNLAFTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAVWVFSLLMSLPLLV--FADVQEGWGTCNLSWPEPVGLWGAAFITYTSVLGFFGPLLVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIMFQ----LEFFMPLGII 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVAAGIV 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKIC------SLKP 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PE---EPTSAGLYFFVVVLSYANSCANPLLYGFLSDNFRQSFRKV-LCLRRGYGMEDADA 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VVSYWPFGSFLCRLVMTLDGINQFTSIFCLMVMSVDRYLAVVHPLRSARWRRPRVAKMAS 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 309.5; DB 2;
Pred. No. 5.4e-21;
3; Mismatches 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIDN: AAB29371.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIDN; AAA17029.1; PID: 9409239
                          PIDN:AAA58255.1; PID:g201059
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PID:g433912
                                                                                                                                                                               human and mouse somatos
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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C;Keywords: G protein-coupled receptor; glycoprotein; hormone F;58-84/Domain: transmembrane #status predicted <TM1> F;95-120/Domain: transmembrane #status predicted <TM2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Yamada, Y.; Post, S.R.; Wang, K.; Tager, H.S.; Bell, G.I.; Proc.-Natl. Acad. Sci. U.S.A. 89, 251-255, 1992
A;Title: Cloning and functional characterization of a family A;Reference number: A41795; MUID:92108031; PMID:1346068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GDB:134185; OMIM:182451
A;Map position: 14q13-14q13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QΥ
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QΥ
                                                                                                                                    F:130-208/Disulfide bonds: #status predicted F:172/Binding site: phosphate (Thr) (covalent) F:265/Binding site: phosphate (Ser) (covalent) F:339/Binding site: palmitate (Cys) (covalent)
                                                                                                                                                                                                                          F;302-326/Domain: transmembrane *status predicted <TM7> \pm \frac{1}{4},44,48,381/Binding site: carbohydrate (Asn) (covalent) *status predicted
                                                                                                                                                                                                                                                                          F;269-296/Domain:
                                                                                                                                                                                                                                                                                             F;220-250/Domain:
                                                                                                                                                                                                                                                                                                                    F;173-195/Domain:
                                                                                                                                                                                                                                                                                                                                       F;132-153/Domain: transmembrane #status predicted <TM3>
                                                                                                                                                                                                                                                                                                                                                                                                                               C; Superfamily: vertebrate rhodopsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Introns: #status absent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Gene: GDB:SSTR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:M81829; NID:g307433; PIDN:AAA58247.1; PID:g307434
A;Note: sequence extracted from NCBI backbone (NCBIN:74767, NCBIP:74768)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-391 < YAM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: A41795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Accession: A41795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 24-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Species: Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  somatostatin receptor 1 - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Keywords: G protein-coupled receptor; hormone receptor; transmembrane protein
                                                                     Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               203 DGTVACNMLMPEPAQRWLVGFVLYTFLMGFLLPVGAICLCYVLIIAKMRMVALKAGWQQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101
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  10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KRSE----RKITLMVMMVVMVFVICWMPFYVVQLVNVFAEQDDAT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GSIVFLTVVAADRYFKVVHPHHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCV-Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CFHMKTWKPSTVYLFNLAVADFLLMICLPFRTDYYLRRHWAFGDIPCRVGLFTLAMNRA 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GACSRGPGSGAADGMEEPGRNASQNGTLSEGQGSAILISFIYSVVCLVGLCGNSMVIYVI 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GSCCRIEGD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RRQQLARQARMKKATRFIMVVAIVFITCYLPSVSARLYFLWTVPSSACDPSVHGALHITL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ETAVSCESFIMESANGWHD----IMFQLEFFMPLGIILFC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TSIYCLTVLSVDRYVAVVHPIKAARYRRPTVAKVVNLGVWVLSLLVILPIVVFSRTAANS
  EGDTISQVMPPLLIVAFV-----LGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85;
                                                                     Similarity
                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                        transmembrane #status predicted <TM4>
transmembrane #status predicted <TM5>
                                                                                                                                                                                                                                                                        transmembrane #status predicted <TM6>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16.6%;
25.7%;
                                                                     16.5%;
26.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     K.; Tager, H.S.; Bell, G.I.; Seino, 9, 251-255, 1992
                                                62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----TISQVMPPLLIVAFV-----LGALGNGVALCGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 307; DB 2; Pred. No. 9.9e-21;
                                                                     Score 305.5;
Pred. No. 1.
                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                295
                                                                     1.4e-20;
                                                                              DB 2;
                                                                                                                                      (by cAMP-dependen)
#status predicted
                                                                                                                                                           (by cAMP-dependent (by cAMP-dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           130;
                                              128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 391
                                                                                        Length
                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                          receptor; lipoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -VSQLSV
                                                37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human
                                                                                                                                                           kinase) #status
kinase) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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В

47 QNGTLSEGQGSAILISFIYSVVCLVGLCGNSMVIYVILRYAKMKTATNIYILNLAIADEL 106

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A;Note: it is uncertain whether Met-1 is the initiator or whether transl R;Li, X.J.; Forte, M.; North, R.A.; Ross, C.A.; Snyder, S.H. J. Biol. Chem. 267, 21307-21312, 1992

A;Title: Cloning and expression of a rat somatostatin receptor enriched A;Reference number: A45102; MUID:93016064; PMID:1400442

A;Accession: A45102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Note: sequence extracted from NCBI backbone (NCBIP:116692) C; Superfamily: vertebrate rhodopsin C; Keywords: G protein-coupled receptor; glycoprotein; recept
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; not compared with conceptual translation A;Molecule type: nucleic acid A;Residues: 1-391 <LII>
VFITCYLPSVSARLYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPK 287
                                                          YTFLMGFLLPVGAICLCYVLIIAKMRMVALKAGWQQRKRSE-----RKITLMVMMVVM
                                                                                                                                                                                    ARYRRPTVAKVVNLGVWVLSLLVILPIVVFSRTAANSDGTVACNMLMPEPAQRWLVGFVL
                                                                                                                                                                                                                                                 VNTISTRVAAGIVCTLWALVILGTVYLLLENHLCV-QETAVSCESFIMESANGWHD----
                                                                                                                                                                                                                                                                                                                                                                                                                                         QNGTLSEGQGSAILISFIYSVVCLVGLCGNSMVIYVILRYAKMKTATNIYILNLAIADEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EGDTISQVMPPLLIVAFV-----LGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFL 63
                                                                                                                                                                                                                                                                                                               LMLSVPFLVTSTL-LRHWPFGALLCRLVLSVDAVNMFTSIYCLTVLSVDRYVAVVHPIKA
                                                                                                                                                                                                                                                                                                                                                                         LMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHA 123
                                                                                                                       -SFKIVWSLRRRQQLARQARMKKATRFIMVVAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 391;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37;
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                A;Molecule type: DNA
A;Residues: 1-369 <YAM>
A;Cross-references: GB:M81830; NID:g307435; PIDN:AAA58248.1; PID:g307436
A;Cross-references extracted from NCBI backbone (NCBIN:74769, NCBIP:74770)
C;GenetLos:
A;Gene: GDB:SSTR2
A;Cross-references: GDB:134186; OMIM:182452
                                                                                                                                                                                                                                           R;Yamada, Y.; Post, S.R.; Wang, K.; Tager, H.S.; Bell, G.I.; Seino, S. Proc. Natl. Acad. Sci. U.S.A. 89, 251-255, 1992
A;Title: Cloning and functional characterization of a family of human and A;Reference number: A41795; MUID:92108031; PMID:1346068
A;Accession: B41795
                                                                                                                                                                                                                                                                                                                                                                                               somatostatin receptor 2 - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 24-Nov-1999 C;Accession: B41795
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A; Map position: 17q24-17q24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         244 LWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 149 CIIIWLLAGLASLPTIIHRNVFFIENTNITYCAFHYESQNSTLPVGLGLTKNILGFLFPF 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LGLIRDCKIEDIVDTAMPITICLAYFNNCLNPLFYGFLGKKFKKYFLQLLKYIPPKAKSH 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -LIILTSYTLIWKTLKKAYEIQKNKPRKDDIFKIILAIVLFFFFSWVPHQIFTFMDVLIQ 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIV--FITCYLP----SVSARLYF 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SNLSTKMSTLSYRPSENGNSSTKKP
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166 124 107

IMFQLEFFMPLGIILFC----

Ωy В Qy Вþ Q

A; Experimental source: brain

Query Match Best Local S Matches 81

Similarity 26.3 81; Conservative

16.5%;

Score 305.5; DB 2 Pred. No. 1.4e-20; Mismatches

DB 2; 128;

62;

47 64

10

Ş Вþ Qγ

228

QY 13/ C-TLWALVILGTYYELL-ENHLCVQETAVSCESEIMESANGWHDIMFQLEFFMPL 189	A; Note: It is uncertain whether Met-1 is the initiator or whether translation is initiat
	A. CLUSS TELETERES. NELACIONAL (GENOLOGO) NID (GOGODY) KIDNICAMA44193.1; KID (GOGOLOGO)
Db 90 MEYRWPFGNYLCKIASASVSFNLYASVFLLTCLSIDRYLAIVHPMKS-RLRRTMLVAKVT 148	A: Residues: 1-391 < MEY>
	A; Molecule type: mRNA
Qy 77 RRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVAAGIV 136	A; Accession: A39297
DD 30 MIPTEYSIIFVVGIEGNSLVVIVIYEYMKIKTVASVEILNLALADECELLTEPLMAVYTA 89	A; Reference number: A39297; MUID:92096119; PMID:1661599
	NA CELL BIOL. 10, 689-694, 1991
Qy 17 VMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMICLPFRTDYYL 76	R; Meyerhof, W.; Paust, H.J.; Schoenrock, C.; Richter, D.
Matches 81; Conservative 68; Mismatches 143; Indels 33; Gaps 8	C;Date: 03-Aug-1992 #sequence_revision 03-Aug-1992 #text_change 24-Nov-1999 C;Accession: A39297; A45102; S20088
Query Match 16.4%; Score 304.5; DB 2; Length 359; Best Local Similarity 24.9%; Pred. No. 1.5e-20;	C:Species: Rattus norvegicus (Norway rat)
	somatostatin receptor - rat
C;Superfamily: vertebrate rhodopsin	A39297
A;Cross-references: GB:X62294; NID:q43; PIDN:CAA44182.1; PID:q44	RESULT 13
A; Molecule type: mRNA A:Residues: 1-359 <sas></sas>	
A; Status: preliminary	Db 333 SFQRI-LC 339
A; Accession: S15403	
A;Title: Cioning and expression of a complementary DNA encoding a bovine adrer A;Reference number: S15403; MUID:91251900; PMID:2041569	QY 288 FYNKLKIC 295
Nature 31, 230-233, 1991	212 AEATCHMEETAAKHANAEUGKANATAOOFPATHOTUNOCUNETHIGE POINE UK 325
) ~·	
C; Accession: S15403	QY 228 VFITCYLPSVSARLYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPK 287
C.Date 19-Mar-1907 #secimence revision 19-Mar-1907 #toyt charics (calcie)	
anglotensin II receptor type I - bovine	Db 226 VTTIMGETI.DVGATOTOVVITTAKMDNVATKAGUOODERSE=BETTIMGATI.DVGATOTOVVITTAKMDNVATKAGUOODERSE=BETTIMGATOTOVOOTOVOOTO
\$15403	OY 179 IMEQLEFEMPLGIILECSEKIVWSLRRRQQLARQARMKKATREIMVVAI 227
RESULT 14	
	Db 166 ARYRRPTVAKVVNLGVWVLSLLVILPIVVFSRTAANSDGTVACNMLKPEPAORWLVGFVL 225
Db 333 SFQRI-LC 339	Qy 124 VNTISTRVAAGIVCTLWALVILGTVYLLLENHLCV-QETAVSCESFIMESANGWHD 178
OV 288 FYNKLKIC 295	Db 107 LMLSVPEVTSTL-LRHWPFGALCRLVLSVDAVNMFTSIYCLTVLSVDRYNAVVHPIKA 165
Db 279 VEVICWMPEYAVQLVNVFAEQDDATVSQLSVILGYANSCANPILYGFLSDNEKR 332	QY 64 LMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHA 123

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A;Introns: #status absent
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; hormone receptor; lipoprotein; phc
F;44-69/Domain: transmembrane #status predicted <TM1>
F;80-105/Domain: transmembrane #status predicted <TM2>
F;117-138/Domain: transmembrane #status predicted <TM3>
F;128-180/Domain: transmembrane #status predicted <TM4>
F;205-235/Domain: transmembrane #status predicted <TM6>
F;204-281/Domain: transmembrane #status predicted <TM6>
F;288-315/Domain: transmembrane #status predicted <TM6>
F;202-29,32,351/Psinding site: carbohydrate (Asn) (covalent) #status predicted
F;315-193/Disulfide bonds: #status predicted
F;315-193/Disulfide bonds: #status predicted
F;328/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predicted
F;328/Binding site: palmitate (Cys) (covalent) #status predicted
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Search completed: March 26, 2003, 19:39:12 Job time : 21 secs
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Best Local S
Matches 90
                                                                                                                      330 VK 331
                                                                                                                                                                                                                                         272 -FYIFNVSSVSMAISPTPALKGMEDEVVVLTYANSCANPILYAFLSDNFKKSFQNV-LCL 329
                                                                                                                                                                                                                                                                        241 LYFLWTVPSSAC----DPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICS 296
                                                                                                                                                                               297 LK 298
                                                                                                                                                                                                                                                                                                                                                                                                  185 FFMPLGIILFCSFKIVWSLR----RQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     160 KMITMAVWGVSLLVILPIMIYAGLRSN---QWGRSSCTINWPGESGAWYTGFIIYTFILG 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101 -MQVALVHWPFGKAICRVVMTVDGINQFTSIFCLTVMSIDRYLAVVHPIKSAKWRRPRTA 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13 TISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMICLPFRT 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41 TSNAVLTFIYFVVCIIGLCGNTLVIYVILRYAKMKTITNIYILNLAIADELFMLGLPFLA 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 29.8 es 90; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                          encoding a putative G protein-coupled receptor.", Genomics 42:519-523(1997).
-!- FUNCTION: ORPHAN RECEPTOR.
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15-JUN-2002 (Rel. 41, Last annotation update)
Probable G protein-coupled receptor GPR31.
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                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                             602043;
                                                                                                                                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KMTGEPDNNRSTSVELTGDPNKT-RGAPEALMANSGEPWSP
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                                                                                                    HGNC:4486; GPR31
       PR00237;
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100
387
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                                                                                                                              AAC51375.1;
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Pred. No. 3.
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BY SIMILARITY.
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                                                                                                                                                                                                                                                  as its content
                                                                                                                                                                                            http://www.isb-sib.ch/announce/
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                                                                  Hui Y., Yang G., Galczenski H., Figueroa D.J., Austin (Copeland N.G., Gilbert D.J., Jenkins N.A., Funk C.D.; "The murine cysteinyl leukotriene 2 (CysLT2) receptor. genomic cloning, alternative splicing, and in vitro characterization.";
                                           J. Biol. Chem. -! - FUNCTION:
                                                                                                                                                   TISSUE-Heart;
                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                  15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
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DOMAIN
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                                                                                                                                   MEDLINE=21601669; PubMed=11591709;
                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                Mus musculus (Mouse)
                                                                                                                                                                                                                                            CYSLTR2 OR CYSLT2
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Biol. Chem. 276:47489-47495(2001).

FUNCTION: Receptor for cysteinyl leukotrienes. The response is mediated via a G-protein that activates a phosphatidylinositol-calcium second messenger system. The rank order of affinities f the leukotrienes is LTC4 = LTD4 >> LTE4.
                                                                                                                                                                                                                                                                                                                                                                                                                                           CLQFVLPFGLIVFCNAGIIRALQKRLREPEKQPKLQRAQALVTLVVVLFALCFLPCFLAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMI 66
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G_PROTEIN_RECEP_F1_2; 1.
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EXTRACELLULAR (POTENTIAL).

5 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

6 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

7 (POTENTIAL).
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(CysLTR2).
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CLT2_HUMAN STANDARI
Q9NS75; Q9HCQ2;
15-JUN-2002 (Rel. 41, 0
15-JUN-2002 (Rel. 41, 1
15-JUN-2002 (Rel. 41, 1
Cysteinyl leukotriene 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
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TISSUE SPECIFICITY: Widely expressed at low levels, with highest expression in the spleen, thymus and adrenal gland, and lower in the kidney, brain and peripheral blood leukocytes.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                    CYLPSVSARLYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSF 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGI:1917336;
                                                                                                                                          CFLPYHALRTLHLVTWDKDSCGDVLHKATVITLTMAAANSCFNPFLYYFAGENF
                                                                                                                                                                                                                        NGWHDIMFQLEFFMPLGIILFCSFKIVWSLRRRQ--QLARQARMKKATRFIMVVAIVFIT
                                                                                                                                                                                                                                                                                                                                                                                          YNGSCCRIEGDTISQYMPPLLIVAFYLGALGNGVALCGFCFHMKTWKPST---VYLFNLA
                                                                                                                                                                                               LIMNHIAVAVGFLLPFLTLTVCYLLIIRILLKAEIPESGPRAAHRKALTTIVIAMITFLL
                                                                                                                                                                                                                                                                               HPHHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSC-----ESFIMESA 173
                                                                                                                                                                                                                                                                                                           TSDFLFISTLPFRADYYFRGSNWIFGDLACRVMSYSLYVNMYTSIYFLTVLSVVRFQATV 125
                                                                                                                                                                                                                                                                                                                                     VADFILMICLPFRIDYYLRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVV
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32.7%;
 Last sequence update)
Last annotation update)
receptor 2 (CysLTR2) (PSEC0146) (HG57) (HPN321)
                                          Created)
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5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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Pred. No. 4.1
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4 (POTENTIAL)
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EMBL;
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-!- FUNCTION: Receptor for cysteinyl leukotrienes. The response is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=20545741; PubMed=11093801; Nothacker H.-P., Wang Z., Zhu Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lynch K.R., Evans J.F.; "Characterization of the human cysteinyl leukotriene 2 receptor."; J. Biol. Chem. 275:30531-30536(2000).
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MEDLINE=20459128; PubMed=10851239;
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Biochem. Biophys. Res. Commun. 274:316-322(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Takasaki J., Kamohara M., Matsumoto M., Saito
Nishikawa T., Kawai Y., Masuho Y., Isogai T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                          use by non-profit institutions as long modified and this statement is not removed.
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                                                                                                                                                                                                                                       s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EM European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                               slightly in smooth muscle cells.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
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TISSUE SPECIFICITY: Widely expressed, with highest levels in heart, placenta, spleen, peripheral blood leukocytes and adregland. In lung, expressed in the interstitial macrophages, an
                                                                                                                                                                                                                                                                                                                                                                                                                    mediated via a G-protein that activates a phosphatidylinositol-calcium second messenger system. Stimulation by BAY u9773, a partial agonist, induces specific contractions of pulmonary veins and might also have an indirect role in the relaxation of the pulmonary vascular endothelium. The rank order of affinities for the leukotrienes is LTC4 = LTD4 >> LTE4.
                                                              C; AB038269; BAB03601.1; -. AF254664; AAG17281.1; -. AF279611; AAK69485.1; -. AL137118; CAC29102.1; -. AB041644; BAB16379.1; -.
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uki Y., Sugano
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InterPro; IPR004071; Cysleuk_receptor.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.

EMBL; AB041644 MIM; 605666; -

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01-FEB-1994
15-DEC-1998
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TRANSMEM
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                                                       NCBI_TaxID=9031;
                                                                                             Archosauria;
                                                                                                               Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                       P2YR_CHICK
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(Rel. 28, Last sequence update)
(Rel. 37, Last annotation update)
eptor 1 (ATP receptor) (P2Y1) (Purinergic receptor).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         receptor;
                                                                                           Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chordata; Craniata; Vertebrata; Euteleostomi;
Neognathae; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                                                                                                                                         308
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N-LINKED (GLCN
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Pred. No. le
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7 (POTENTIAL).
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6 (POTENTIAL
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                                                                                       Phasianinae;
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Best Local
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PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

G-protein coupled receptor; Transmembrane; Glycoprotein; 3D-structure.

DOMAIN 1 41 EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as rung _____sage by and for commodified and this statement is not removed. Usage by and for commodified and this statement is not removed. Usage by and for commodified and this statement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                   SEQUENCE
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PDB; 1DDD; 11-JUL-96.
InterPro; IPR000276; GPCR_Rhodpsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  van Rhee A.M., Fischer B., van Galen P.J.M., Jacobson K.A.; "Modelling the P2Y purinoceptor using rhodopsin as template."; Drug Des. Discov. 13:133-140(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEBS Lett. 324:219-225(1993).
[2]
3D-STRUCTURE MODELING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=93285340; PubMed=8508924; Webb T.E., Simon J., Krishek B.J., Bateson King B.F., Burnstock G., Barnard E.A.;
    103
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                             78
                                                        43
                                                                  IG DES. DÍSCOV. 13:133-140(1995).

FUNCTION: RECEPTOR FOR EXTRACELLULAR ADENINE NUCLEOTIDES SUCH AS FUNCTION: RECEPTOR FOR EXTRACELLULAR ADENINE NUCLEOTIDES SUCH AS ATP AND ADP. SEEMS TO MEDIATE ITS ACTION VIA A PERTUSSIS TOXIN INSENSITIVE G-PROTEIN, PROBABLY BELONGING TO THE GQ FAMILY THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM. SUBCELLULAR LOCATION: Integral membrane protein.

TISSUE SPECIFICITY: BRAIN, SPINAL CORD, GASTROINTESTINAL TRACT, SPLEEN AND LEG MUSCLE. IS NOT DETECTED IN THE HEART, LIVER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
KTDWIFGDVMCKLQRFIFHVNLYGSILFLTCISVHRYTGVVHPLKSLGRLKKKNAVYVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STOMACH,
                       RRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVAAGIVC
                                                     LPTVYILVFITGELGNSVAIWMEVEHMRPWSGISVYMENLALADELYVLTLPALIFYYEN 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PR00237; GPCRRHODOPSN
                                                                                                                          Similarity
                                                                                                                                                                   362 AA;
                                                                                                              Conservative
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116
137
156
178
208
228
255
275
293
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                                                                                                                                                                              41194 MW;
                                                                                                                         19.6%;
29.1%;
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                                                                                                         Score 364; DB
Pred. No. 1.5e
58; Mismatches
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N-LINKED (GLC)
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2 (POTENTIAL
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                                                                                                                         DB 1;
..5e-18;
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                                                                                                                                                                                        (POTENTIAL)
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RESULT 6
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ID PAYEL
AC P49652
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DT 01-
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PIAM; PF00001; 7tm.1; 1.

PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; GPROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane;
DOMAIN

1

41

EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The 6H1 orphan receptor, claimed to be the p2y5 receptor, does not mediate nucleotide-promoted second messenger responses."; Biochem. Biophys. Res. Commun. 236:455-450(1997).

-I-FUNCTION: RECEPTOR FOR EXTRACELLULAR ADENINE NUCLEOTIDES SUCH AS ATP AND ADP. SEEMS TO MEDIATE ITS ACTION VIA A PERTUSSIS TOXIN INSENSITIVE G-PROTEIN, PROBABLY BELONGING TO THE GQ FAMILY THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for an entitles requires a license.
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                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/
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15-JUL-1998 (Rel. 36, Last annotation update)
P2Y purinoceptor 1 (ATP receptor) (P2Y1) (Purinergic receptor) (6H1
                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE=97382456; PubMed=9240460;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     phospholipase C. Mol. Pharmacol.
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Filtz T.M., Li Q., Boyer J.L., Nicholas R.A., Harden T.K.;
"Expression of a cloned P2Y purinergic receptor that couples
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Brain;
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Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P49652;
01-FEB-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                          ween the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are no reby non-profit institutions as long as its conten
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: MAINLY FOUND IN BLOOD, BRAIN, AND LUNG. TO
LESSER EXTENT IN STOMACH, GUT, AND SKELETAL MUSCLE.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATRKSSRRSEP -- NVQSKSEEMTLNIL 351
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                                                                                                                                                                                                                     AF012103; AAF
P34996; 1DDD.
                                                                                                                                                                                                                                                                                U09842; AAA18784.1;
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                                                                                                                                                                                                                                                                                                                                   an email to license@isb-sib.ch).
                                                                                                                                                                                     IPR000276; GPCR_Rhodpsn
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                                                                                                                                                                                                                                                 AAB65428.1; -.
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33, Last sequence update)
36, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Common turkey).
Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Galliformes; Meleagrididae; Meleagris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nicholas R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             362
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      Glycoprotein. (POTENTIAL).
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RESULT 7
P2YR_BOVIN
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Best Local
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                                                                                                                                                                                                                       P2YR_BOVIN
P48042;
                                                                                                                                                                     01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
P2Y purinoceptor 1 (ATP receptor) (P2Y1) (Purinergic receptor).
                  Henderson D.J., Elliot D.G., Smith G.M., Webb T.E., Dainty I.A., "Cloning and characterisation of a bovine P2Y receptor."; Biochem. Biophys. Res. Commun. 212:648-656(1995).
                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
SEQUENCE FROM N.A.
                                                       TISSUE=Aortic endothelium; MEDLINE=95352058; PubMed=7626079;
                                                                              SEQUENCE FROM
                                                                                                                  Bovidae;
                                                                                                                                                  Bos taurus (Bovine).
                                                                                                                                                                P2RY1
                                                                                                      NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                            ATRKSSRRSEP -- NVQSKSEEMTLNIL 351
                                                                                                                                                                                                                                                                                                                  LKICSLKPKQPGHSKTQRPEEMPISNL 318
                                                                                                                                                                                                                                                                                                                                       {\tt MKTLNLRARLDF-QTPQMCAFNDKVYATYQVTRGLASLNSCVDPILYFLAGDTFRRRLSR}
                                                                                                                                                                                                                                                                                                                                                                                                                                 LVWALVVAVIAPILFYSGTGVRRNKTITCYDTTADEYLRSYFVYSMCTTVFM------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LPTVYILVFITGFLGNSVAIWMFVFHMRPWSGISVYMFNLALADFLYVLTLPALIFYYFN 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMICLPFRTDYYLR 77
                                                                                                                                                                                                                                                                                                                                                              ----SVSARLYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNK
                                                                                                                                                                                                                                                                                                                                                                                                           IMFQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLP---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVAAGIVC 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                              Bovinae;
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                                                                                                                 Bos.
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29.1%;
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N-LINKED (GLCNAC. . .)

N-LINKED (GLCNAC. . .)

N-LINKED (GLCNAC. . .)

N-LINKED (GLCNAC. . .)
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CYTOPLASMIC (F
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EXTRACELLULAR (POTENTIAL)

3 (POTENTIAL)
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CYTOPLASMIC (
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6 (POTENTIAL
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5 (POTENTIAL)
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4 (POTENTIAL
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7 (POTENTIAL).
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                                                                                                                                                                                                                                   373 AA
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            corpus callosum.";
Neurobiol. Dis. 5:259-270(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Deng G., Matute C., Kumar C.K., Fogarty D.J., Miledi R.; "Cloning and expression of a P2y purinoceptor from the adult bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Corpus callosum; MEDLINE=99064562; PubMed=9848096;
                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
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                                                                                                                                                                                                                                               18 MPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMICLPFRTDYYLR 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                         RRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVAAGIVC 137
                                                                                                                                                                                                                     LPAVYILVFIIGFLGNSVAIWMFVFHMKPWSGISVYMFNLALADFLYVLTLPALIFYYFN 113
                            LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300
                                                                                                           LVWLIVVVGISPILFYSGTGIRKNKTITCYDTTSDEYLRSYFIYSM-----CTTVAMFCV
                                                                                                                                     TLWALVILGTVYLLLENHLCVQET-AVSC------ESFIMESANGWHDIMFQLEFFM 187
                                                                                                                                                               KTDWIFGDAMCKLQRFIFHVNLYGSILFLTCISAHRYSGVVYPLKSLGRLKKKNAVYISV 173
 LDF-QTPEMCAFNDRVYATYQVTRGLASLNSCVDPILYFLAGDTFRRRLSR---
                                                       PLVLILGCYGLIVRALIYK-DLDNSPLRRKSIYLVIIVLTVFAVSYIPFHVMKTMNLRAR
                                                                                PLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLP-----SVSAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P34996;
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                                                                                                                                                                                                                                                                           92;
                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 coupled
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75
110
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AAC78275.1; -.
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                                                                                                                                                                                                                                                                                      19.6%;
27.5%;
                                                                                                                                                                                                                                                                           68;
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CYTOPLASMIC (POTENTIAL)
4 (POTENTIAL)
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BY SIMILARITY
N-LINKED (GLCNA
N-LINKED (GLCNA
N-LINKED (GLCNA
N-LINKED (GLCNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transmembrane;
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Pred. No. 2e
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5 (POTENTIAL).
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3 (POTENTIAL).
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7 (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                                                                                                                                                        2e-18;
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                                                                                                                                                                                                                                                                           140;
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                                                                                                                                                                                                                                                                                                  Length 373;
                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL)
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RESULT 8
CLT2_PIG
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                                            Query Match
Best Local
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Cysteinyl leukotriene receptor 2 (CysLTR2).
CYSLTR2 OR CYSLT2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kamohara M., Takasaki J., Matsumoto M., Matsumoto S., Saito Ohishi T., Soga T., Matsushime H., Furuichi K.; "Characterization of the cloned rat and porcine cysteinyl le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Receptor for cysteinyl leukotrienes. The response is mediated via a G-protein that activates a phosphatidylinositol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sus scrota (Pig).
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                                                                                                                                                  CARBOHYD
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                                                                                         SEQUENCE
                                                                                                                       CARBOHYD
                                                                                                                                       CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                            G-protein
                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS50262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AB052662; BAB60817.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9823;
                                                                                                         CARBOHYD
                                                                                                                                                                     DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            338 -- ATRKASRRSEANLQSKSEDMTLNILSEFKQNGD 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301 QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSD 335
 19 PPLLIVAFVLGALGNGVALCGFCFHMKTWKPST---VYLFNLAVADFLLMICLPFRTDYY 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  calcium second messenger system (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PF00001; 7tm_1;
                             86;
                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                            coupled receptor; Transmembrane; Glycoprotein
                                                                                         345 AA;
                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                           G_PROTEIN_RECEP_F1_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                          G_PROTEIN_RECEP_F1_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cetartiodactyla; Suina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chordata; Craniata; Vertebrata;
                                                                                         39410 MW;
                                            19.5%;
                               59;
                                                                                                      N-LINKED (GLCNAC...) (POTENTIAL)
N-LINKED (GLCNAC...) (POTENTIAL)
N-LINKED (GLCNAC...) (POTENTIAL)
N-LINKED (GLCNAC...) (POTENTIAL)
                                                                                                                                                                  7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
                                                                                                                                                                                                                              CYTOPLASMIC (
                                                                                                                                                                                                                                                          EXTRACELLULAR (POTENTIAL)
5 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                  2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                             Pred.
                                                           Score 362;
                                                                                                                                                                                                   EXTRACELLULAR (POTENTIAL)
7 (POTENTIAL).
                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                      (POTENTIAL)
                                                                                           5D1B1FB89BB95905 CRC64;
                                 Mismatches
                                             No.
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                                             2e-18
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                                 118;
                                                          Length 345;
                                 Indels
                                                                                                                                                    (POTENTIAL)
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                                                                                                                                                             InterPro; 1:...

Pfam; PF00001; 7tm_1; 1.

Pfam; PF00001; 7tm_1; 1.

PRINTS; PR00237; GPCRRHODOPSN.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_1; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

PROSITE; PS50262; 
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                                                              TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-95298025; PubMed=7779087;
Tokuyama Y., Hara M., Jones E.M.C., Fan Z., Bell G.I.;
"Cloning of rat and mouse P2Y purinoceptors.";
Biochem. Biophys. Res. Commun. 211:211-218(1995).
-!- FUNCTION: RECEPTOR FOR EXTRACELLULAR ADENINE NUCLEOTIDES SUCH AS ATP AND ADP. IN PANCREATIC ISLETS, MAY MEDIATE SOME OF THE EFFECT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
P2Y purinoceptor 1 (ATP receptor) (P2Y1) (Purinergic receptor).
        DOMAIN
                                                                                                                         DOMAIN
                                                                                                                                                    TRANSMEM
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OF EXTRACELLULAR ATP ON INSULIN SECRETION.
SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: EXPRESSED IN MUSCLE, HEART, LIVER, KIDNEY,
LUNG, BRAIN, SPLEEN, BUT NOT IN TESTIS.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  U22830; AAA91303.1; P34996; 1DDD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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     receptor;
52
74
87
109
126
147
166
188
218
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                      CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
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CLT2_RAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLT2_RAT STANDARD; PRT; 309 AA. 0924T9; 0924T9; 15-JUN-2002 (Rel. 41, Created) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) 15-JUN-2002 (Rel. 41, Last annotation update) Cysteinyl leukotriene receptor 2 (CystTR2) (RSBPT32).
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CARBOHYD
                                                                                                                                                                                                                               -i- FUNCTION: Receptor for cysteinyl leukotrienes. The response is mediated via a G-protein that activates a phosphatidylinositol-calcium second messenger system (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                         Kamohara M., Takasaki J., Matsumoto M., Matsumoto S., Saito T., Ohishi T., Soga T., Matsushime H., Furuichi K.; "Characterization of the cloned rat and porcine cysteinyl leuko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYSLTR2 OR CYSLT2.
                                                           the European Bioinformatics Institute.
                                                                                              between
                                                                                                                                                                                                                                                                                                                                Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18 MPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMICLPFRTDYYLR 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                             SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                 SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LVWLIVVVAISPILFYSGTGIRKNKTVTCYDSTSDEYLRSYFIYSM-----CTTVAMFCI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LYFLWTVPSSACD--PSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LDF---QTPEMCDFNDRVYATYQVTRGLASLNSCVDPILYFLAGDTFRRRLSR-----
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   non-profit institution and this statement is
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                               institutions as long
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27.0%;
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                                                                                                                                                                                                                                                                                                                                                                                      cloned rat and porcine cysteinyl leukotriene
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CYTOPLASMIC (POTENTIAL).

BY SIMILARITY

N-LINKED (GLCNAC...) (POTENTIAL).

MGLTMKED (GLCNAC...) (POTENTIAL).
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Pred. No. 3.8
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CYTOPLASNIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
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Sciurognathi; Muridae; Murinae; Rat
not removed.
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                      There are no restrictions ong as its content is in
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for commercial
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                                                                                                                                                                                                            RESULT 11
P2YR_HUMAN
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
CARBOHYD
TISSUE=Placenta;
MEDLINE=96257237;
Leon C., Vial C.,
                                                                                                                               01-FBB-1996 (Rel. 33, Created)
01-FBB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
P2Y purinoceptor 1 (ATP receptor) (P2Y1) (Purinergic receptor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                             Eukaryota; Metazoa; Mammalia; Eutheria;
                                                                                                                                                                                   P2YR_HUMAN P47900;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
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                                        SEQUENCE FROM N.A.
                                                                NCBI_TaxID=9606;
                                                                                                     Homo sapiens (Human)
                                                                                                                       P2RY1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YSDKNCTIE-NEKRDEYPIIYLIIEVWGALGNGESIYVE---LQTYKKSTSVNVEMLNLA
                                                                                                                                                                                                                                                                 LPYHALRTIHLVTWDADSCMDELHKATVITLTLAAANSCFNPFLYYFAGENF 296
                                                                                                                                                                                                                                                                                                                                                                                                                                              VADFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVV 118
                                                                                                                                                                                                                                                                                        LPSVSARLYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSF
                                                                                                                                                                                                                                                                                                                 LNYIALGVGFLLPFFILTICYLLIIRVLLKVEIPESGPRDAQRKALTTIVIAMIIFLLCF
                                                                                                                                                                                                                                                                                                                                          WHDIMFQLEFFMPLGIILFCSFKIVWSLRRRQ--QLARQARMKKATRFIMVVAIVFITCY
                                                                                                                                                                                                                                                                                                                                                                     HPFQMLHITSVR-SAWILCGIIWVFIMASSGLLLKHGQEKKNNTTLCFELNLQKFKNLVI 184
                                                                                                                                                                                                                                                                                                                                                                                            HPHHAVNTISTRVAAGIVC-TLWALVILGTVYLLLENHLCVQETAVSCESFIMESAN--G
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                                                                                                                                                                                                 STANDARD;
 PubMed=8666290;
Cazenave J.-P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       receptor; Transmembrane;
                                                                               Primates;
                                                                                         Chordata;
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31.2%;
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Pred.
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5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
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BY SIMILARI
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7 (POTENTIAL).
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4 (POTENTIA
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                                                                              Catarrhini;
                                                                                            Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                 PRT;
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-LINKED (GLCNAC. ..) (POTENTIAL)
-LINKED (GLCNAC. ..) (POTENTIAL)
A122AC8177879D56 CRC64;
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  Gachet C.;
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                                                                              Hominidae;
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                                                                                                                                                                                                                                                                                                                   244
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    TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=98113162; PubMed=9442040;
Jin J., Daniel J.L., Kunapuli S.P.;
"Molecular basis for ADP-induced platelet activation. II. The P2Y1
                                                                                                                                                                                                                                                                                                                                                                                             This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   receptor mediates ADP-induced intracellular calcium mobilization shape change in platelets.";
J. Biol. Chem. 273:2030-2034(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=96158962; PubMed=8579591;
                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                              modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                         use
                                                                                                                                                                                                                                                                                                                                                                     the
                                                                                                                                                                                                                                                                                                                                                                                                                                                           <del>-</del> ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Leon C., Vial C., Weber J., Cazenave J.-P., Gacher C.; Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Cloning and tissue distribution Biochem. Biophys. Res. Commun.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=96205320; PubMed=8630005; Janssens R., Communi D., Pirotton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biochem. Biophys. Res. Commun.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        purinoceptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kunapuli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ayyanathan K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gene 171:295-297(1996).
                            DOMAIN
                                        TRANSMEM
                                                    DOMAIN
                                                                  TRANSMEM
                                                                               DOMAIN
                                                                                            Blood coagulation.
                                                                                                      G-protein
                                                                                                                   PROSITE; PS00237; PROSITE; PS50262;
                                                                                                                                               PRINTS;
                                                                                                                                                        Pfam; PF00001; 7tm_1;
                                                                                                                                                                       InterPro;
                                                                                                                                                                                     MIM; 601167;
                                                                                                                                                                                                 Genew;
                                                                                                                                                                                                            HSSP; P34996;
                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                       EMBL;
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                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                  between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Platelet;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 95-373 FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Boeynaems J.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Cloning and chromosomal localization of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              purinoceptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Cloning and sequencing
                                                                                                                                                                                                                                                                                                                                                                 SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                            CHANGE IN PLATELET SHAPE, AND PROBABLY TO PLATELET SUBCELLULAR LOCATION: Integral membrane protein. INDUCTION: REPRESSED BY THE P2Y1 RECEPTOR-SPECIFIC A3P5PS, A3P5P AND A2P5P. THESE INHIBIT CALCIUM ION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: RECEPTOR FOR EXTRACELLULAR ADENINE NUCLEOTIDES SUCH AS ATP AND ADP. IN PLATELETS BINDING TO ADP LEADS TO MOBILIZATION O INTRACELLULAR CALCIUM IONS VIA ACTIVATION OF PHOSPHOLIPASE C, A
                                                                                                                                                                                                                                                                                                                                                                                                                    AND SHAPE CHANGE IN PLATELETS.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                ;; Z49205; CAA89066.1;
;; U42030; AAA97873.1;
;; U42029; AAA97872.1;
;; S81950; AAB47091.1;
                                                                                                                                                                                                                           AF018284; AAB94556.1;
                                                                                                                                                                                                                                      AJ006945; CAA07339.1;
                                                                                                                                                                                                HGNC:8539; P2RY1
                                                                                                                                            PR00237; GPCRRHODOPSN
                                                                                                                                                                                                                                                                                                                                                         non-profit
                                                                                                      coupled
                                                                                                                                                                       IPR000276; GPCR_Rhodpsn
                                                                                                                                                                                                             IDDD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tania W.,
                                                                                                                   G_PROTEIN_RECEP_F1_1; 1.
G_PROTEIN_RECEP_F1_2; 1.
                                                                                                        receptor;
  52
74
87
109
126
147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      distribution of the human P2Y es. Commun. 221:588-593(1996).
                                                                                                                                                                                                                                                                                                                                                         institutions as long
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                        Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human cDNA encoding endothelial P2Y1
                                                               EXTRACELLULAR (POTENTIAL).
1 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              218:783-788(1996)
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                                                                                                                                                                                                                                                                                                                                                       as its content
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                                                                                                                                                                                                                                                                                                                                           Usage by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P2Y1 receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Parmentier M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOBILIZATION
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                                                                                                          Platelet;
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P2YR_MOUSE
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Best Local
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01-FEB-1996
01-FEB-1996
15-JUN-2002
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DOMAIN
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"Thromboresistance in P2Y1 receptor knockout mice.";
Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
-i-FUNCTION: RECEPTOR FOR EXTRACELLULAR ADENINE NUCLEOTIDES SUCH AS
ATP AND ADP. IN PANCREATIC ISLETS, MAY MEDIATE SOME OF THE EFFECT
                                                           SEQUENCE FROM N.A. STRAIN=129/Sv;
                                                                                              MEDLINE-95298025; PubMed-7779087;
Tokuyama Y., Hara M., Jones E.M.C., Fan Z., Bell
"Cloning of rat and mouse P2Y purinoceptors.";
Biochem. Biophys. Res. Commun. 211:211-218(1995).
                                                                                                                                           TISSUE=Insulinoma;
                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                        P2YR_MOUSE
                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                     Mus musculus (Mouse).
                                                                                                                                                                                                                                   P2RY1
                                                 Leon C.
                                                                                                                                                                                                                                                                                                                                                                   344 RRSEANLQSKSEDMTLNIL 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               114 KTDWIFGDAMCKLQRFIFHVNLYGSILFLTCISAHRYSGVVYPLKSLGRLKKKNAICISV 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            purinoceptor
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                                                                                                                                                                                                                                                                                                                                                                                       QPGHSKTQ-RPEEMPISNL 318
                                                                                                                                                                                                                                                                                                                                                                                                                                         LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLP-----SVSAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TLWALVILGTVYLLLENHLCVQET-AVSC------ESFIMESANGWHDIMFQLEFFM 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVAAGIVC
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189
219
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266
286
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1124
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1138
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(Rel. 33, Last sequence update)
(Rel. 41, Last annotation update)
eptor 1 (ATP receptor) (P2Y1) (Purinergic
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218
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42071
                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                              Chordata;
Rodentia;
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29.2%;
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N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
MISSING (IN REF. 1).
; 4DC7C668B4145392 CRC64;
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N-LINKED
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5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
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Pred. No. 7
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CYTOPLASMIC (POTENTIAL).
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7 (POTENTIAL).
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                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                         PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                         373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
7.8e-18;
                                                                                                                                                                                                                                                                                                         AA
                                                                                                              Bell G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 373;
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                                                                                                                                                                                                                                           receptor).
 EFFECTS
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Best Local
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DOMAIN
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SEQUENCE
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U22829; AAA91302.1; -. EMBL; AJ245636; CAB57317.1; HSSP; P34996; IDDD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00237; GPCRRHODOPSN.
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Pfam; PF00001; 7tm_1; 1.
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338
                     301
                                            290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OF EXTRACELLULAR ATP ON INSULIN SECRETION.
SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    European Bioinformatics Institute. The by non-profit institutions as long
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                                                                                                                                                                                                                                 LPAYYILVFIIGFLGNSVAIWMFVFHMKPWSGISVYMFNLALADFLYVLTLPALIFYYFN 113
                                                                                                                                                                                                                                             MPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMICLPFRTDYYLR
--ATRKASRRSEANLQSKSEEMTLNILSEFKQNGD
                     QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSD
                                                                                         VLILGCYGLIVKAL-IYNDLDNSPLRRKSIYLVIIVLTVFAVSYIPFHVMKTMNLRARLD
                                                                                                                GIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLP-----
                                                                                                                                       LVWLIVVVAISPILEYSGTGTRKNKTVTCYD---TTSNDYLRSYFIYSMCTTVAMFCIPL
                                                                                                                                                            TLWALVILGTVYLLLENHLCVQET-AVSCESFIMESANGWHDIMFQLE-----FFMPL
                                                                                                                                                                                     KTDWIFGDAMCKLQRFIFHVNLYGSILFLTCISAHRYSGVVYPLKSLGRLKKKNAIYVSV 173
                                                                  FLWTVPSSACD--PSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK
                                                                                                                                                                                                         RRHWAFGDIPCRYGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVAAGIVC
                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PS00237;
                                            QTPEMCDFNDRVYATYQVTRGLASLNSCVDPILYFLAGDTFRRRLSR
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113
197
373 AA;
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189
                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                        receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G_PROTEIN_RECEP_F1_1; 1.
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                                                                                                                                                                                                                                                                                         19.0%;
27.2%;
                                                                                                                                                                                                                                                                                                                            WW;
                                                                                                                                                                                                                                                                               66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transmembrane;
                                                                                                                                                                                                                                                                              Score 351.5; DB 1
Pred. No. 1.2e-17;
6; Mismatches 143
                                                                                                                                                                                                                                                                                                                                                 N-LINKED
                                                                                                                                                                                                                                                                                                                           N-LINKED (GLCNAC. . .) (F 944125E9F4560BB3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EXTRACELLULAR (POTENTIAL).

1 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                        N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY
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CYTOPLASMIC (
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biochem, Biophys. Res. Commun. 236:106-112(1997).

-!- SUBCELLULAR LOCATION: Integral membrane protein.

-!- TISSUE SPECIFICITY: NOT DETECTED IN THE BRAIN REGIONS THALAMUS,

-!- TISSUE SPECIFICITY: NOT DETECTED IN THE BRAIN REGIONS THALAMUS,

-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               O'Dowd B.F., Nguyen T., Jung B.P., Marchese A., Cheng Heng H.H.Q., Kolakowski L.F. Jr., Lynch K.R., George "Cloning and chromosomal mapping of four putative nov G-protein-coupled receptor genes."; gene 187:75-81(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q99677; O15132; O1-NOV-1997 (Rel. 35, Created)
O1-NOV-1997 (Rel. 35, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
P2Y purinoceptor 9 (P2Y9) (Purinergic receptor GPR23) (P2Y5-like receptor).
GPR23 OR P2RY9.
                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00001; 7tm_1; 1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=97366605; PubMed=9223435;
Janssens R., Boeynaems J.M., Godart M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

Bohm S.K., Khitin L.M.,

Submitted (JUL-1997) to
           DOMAIN
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P2Y9_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           U66578; AAC51301.1; -. U90323; AAB62087.1; -. U90322; AAB62088.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P34996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AF005419; AAB66322.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HGNC:4478; GPR23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                        receptor; Transmembrane;
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CYTOPLASMIC (POTENTIAL).

2 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

3 (POTENTIAL).

4 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

5 (POTENTIAL).

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6 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

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CYTOPLASMIC (POTENTIAL).

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CYTOPLASMIC (POTENTIAL).

CYTOPLASMIC (POTENTIAL).
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Best Local
                                                         use by non-profit institutions as long a modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                MEDLINE=93329058; PubMed=8393036;
Kaplan M.H., Smith D.I., Sundick R.S.;
"Identification of a G protein coupled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
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                                                                                                                                                                                                This
                                                                                                                                                                                                                       -!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- TISSUE SPECIFICITY: INDUCED IN ACTIVATED T-CELLS.
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gallus gallus (Chicken).
Eukaryota; Metazoa; Chor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation updat
P27 purinoceptor 5 (P2Y5) (Purinergic recep
                                                                                                                                                  the European
                                                                                                                                                                                                                                                                                    J. Immunol. 151:628-636(1993)
-!- SUBCELLULAR LOCATION: Inte
                                                                                                                                                                                                                                                                                                                                T cells."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Archosauria; Aves;
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                                                                                                                                             SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the Eleuropean Bioinformatics Institute. There are no rest
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Neognathae; Galliformes; Phasianidae; Phasiani
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Pred. No. 2.5e-17;
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Mismatches
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c receptor
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                                                                             (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                  receptor induced
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                                                                                                                           as its content
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(POTENTIAL)
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L06109; P34996;

AAB06587.1; 1DDD.

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GP17_HMAN
ID GP17_
AC Q1330
DT 15-JU
DT 15-JU
DT 15-JU
DT Proba
GN GPR17
OS HOMO
OC EUKAR
OC Mamma
OX NCBI_
RN [1]
RP SEQUE
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TRANSMEM
                                                                                                                                                                                                                                                                                 GP17_HUMAN STANDARD; PRT; 367 AA.
Q13304; Q9UDZ6; Q9UEZ1;
Q1-NOV-1997 (Rel. 35, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Probable P2Y purinoceptor GPR17 (P2Y-like receptor) (R12).
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                                                                            Raport C.J., Schweicka
Godiska R., Gray P.W.;
                                                                                                SEQUENCE FROM N.A. (ISOFORM 2).
MEDLINE=96145150; PubMed=8558062;
Raport C.J., Schweickart V.L., Ch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
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PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSMEM
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  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                               Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24 VAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMICLPFRTDYYLRRRHWAF
                                      ew members of the chemokine receptor Leukoc. Biol. 59:18-23(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INCSVVTAVRTMYPVTLCIAVSNCCFDPIVYYFTSDTNSE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPKQPGHSKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LFCSFKIVWSLRRRQQLAR-QARMKKATRFIMVVAIVFITCYLP-SVSARLYFLW---TV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VILGTV----YLLLENHLCVQETAVSCESFIMESANGWHDIMFQL------EFFMPLGII 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVAAGIVC-TLWAL
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  (ISOFORMS 1 AND 2).
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30.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transmembrane; Glycoprotein; Lipoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 339;
Pred. No. 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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4214E969633B6F7D CRC64;
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7 (POTENTIAL).
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                                                                                                    D.,
                                                           gene
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7.1e-17;
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                                                                                                    Eddy R.L. Jr.,
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                                                             family.";
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J. Neurochem. 70:1357-1365(1998).
-!- FUNCTION: Putative receptor for purines coupled to G-proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U33447; AAB16746.1; --
EMBL; Y12546; CAA73144.1; --
EMBL; Z94154; CAB08107.1; --
EMBL; Z94155; CAB080108.1; --
EMBL; Z94155; CAB080108.1; --
EMBL; Z94196; IDDD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      similarity).

1. SUBCELLULAR LOCATION: Integral membrane protein.

1. ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are produced by alternative splicing.

1. TISSUE SPECIFICITY: PRIMARILY EXPRESSED IN BRAIN.

1. SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               G-protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PFAM: PF00001; 7tm 1; 1.

PRINTS; PR00237; GPCRRHODOPSN.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Hippocampus; MEDLINE=98181695; P
                                                                                                                                                                                                    SEQUENCE
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 168
                        127
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                                                VLPTRLVYHESGNHWPFGEIACRLTGFLFYLNMYASIYFLTCISADRFLAIVHP----VKS
                                                                                                                         CRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMI 66
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LKLRRPLYAHLACAFLWVVVAVAMAPLLVSPQTVQTNHTVVCLQLYREKASHHALVSLAV
                                                                CLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNT
                                                                                                  CGQETPLENMLFASFYLLDFILALVGNTLALWLFIRDHKSGTPANVFLMHLAVADLSCVL
                       ISTR--VAAGIVCT-LWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIMFQL
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Q8tds5 homo saplen
Q9ng20 homo saplen
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Q8r528 mus musculu
Q8g944 carassius a
Q9de05 raja erinac
Q90x57 xenopus lae
Q9dg96 carassius a
Q9h1c0 homo saplen
Q9nul ovis aries
Q96ge0 homo saplen
Q96tf2 homo saplen
Q96tf2 homo saplen
Q95ks6 ovis aries
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on incertio, tendossio, seculumospan.	Interpro. IBB00076.	HSSP: P34996: 1DDD.	EMBI: ABOB3631.	EMBL; AF411110; AAL26481.1;	EMBL;	Submitted (APR-	genome sequence.	TACELLETTE OF OF DETOCATE CONFERS TOOM	"Identification of G protein-counled recentor genes from the	Takeda S.			genes.";	"Discovery and mapping of ten novel G pro	Lewis T., Evans J.F., George S.R., O'Dowd B.F.;	RA Lee D.K., Nguyen T., Lynch K.R., Cheng R., Vanti W.B., Arkhitko O.,	MEDLINE=2		[2]	Submitted	chemokine receptor.";	"Molecular	Wang Y			NCBI_TaxID=9606;	Mammalia; Eutheria; Primates;		OS Homo sapiens (Human).	FKSG80 OR	G-protein coupled receptor).	Putative chemokine receptor (G pi	01-JUN-2002 (TrEMBLrel. 21, Last	01-JUN-2001 (01-JUN-2001 (TrEMBLrel.	AC Q9BXC0;	ID Q9BXC0 PRELIMINARY; PRT; 346 AA.	RESULT 1

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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                  Takeda S., Kadowaki S., Haga T., Takaesu H., Mitaku S.; "Identification of G protein-coupled receptor genes fro genome sequence."; Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases EMBL; AB083632; BAB89345.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q8TDS4;
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PROSITE; PS00237; G_PROTEIN_RECEP_F1_1;
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
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NTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIMFQLE
                                               IICLPFLMDNYVRRWDWKFGDIPCRLMLFMLAMNRQGSIIFLTVVAVDRYFRVVHPHHAL
                                                                                                                                         NCCVFRDDFIVKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWKSSRIFLFNLAVADFLL
                                                                                                                                                                   SCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DF1LMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA
                                                                                                                                                                                                                                     180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PF00001; 7tm_1; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G-protein
                                                                                                                                                                                                                                                                                                                          363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 346 AA;
                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                          AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lrel. 21, Created)
Lrel. 21, Last sequence update)
Lrel. 21, Last annotation update)
coupled receptor.
                                                                                                                                                                                                                                                                                                                          41849 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39295 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chordata;
                                                                                                                                                                                                                                                   47.7%;
52.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score No.
                                                                                                                                                                                                                                  47;
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                                                                                                                                                                                                                                                   Score 883.5;
Pred. No. 6e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1853;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                          C4B0EEC9CCB81D56 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E0DB114EEB3A47A5 CRC64;
                                                                                                                                                                                                                                  Mismatches
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                                                                                                                                                                                                                                                No.
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                                                                                                                                                                                                                                                        6e-79;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A
                                                                                                                                                                                                                                                                          DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4;
                                                                                                                                                                                                                                  107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         the
                                                                                                                                                                                                                                7;
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    184
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242 250

YELWIYDS---SACD--PSVHGALHITLSFTYMISMLDPL/VYFSSPSFPKFYKLKICS
RIFWLLYKYNVRNCDIYSSVDLAFFTTLSFTYMISMLDPVVYYFSSPSFPNFFSTCINRC

182 191

241

181

249

LLEFFLPLAIILFCSGRIIWSLRQR-QMDRHAKIKRAINFIMVVAIVFIICFLPSVAVRI

131

122

62 71

FLLIICLPFLTDNYVHNWDWRFGGIPCRVMLFMLAMNRQGSIIFLTVVAVDRYFRVVHPH 130

FLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPH 121

HAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIMF

HFLNKISNRTAAIISCFLWGLTIGLTVHLLYTNMMTKNGEAYLCSSFSICYNFRWHDAMF

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RESULT 3
QUEPG 
ID OUEP 
AC QUEP 
AC QUEP 
AC QUEP 
AC QUEP 
DT 01.M 
DT 01.M 
DT 01.M 
DT 01.M 
DT 01.M 
CC ENKA 
CC MAMM 
CC STRA 
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CT "PUM 
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CC -!-
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                                                                                                                      Query Match
Best Local S
Matches 178
                                                                                                                                                                                                                                          InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRRHODDPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Glycoprotein; R
G-protein coupled receptor; Glycoprotein; R
SEQUENCE 360 AA; 41400 MW; CCCE52A24757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           member of the seven transmembrane spanning superfamily.";
submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
EMBL; AJ300199; CAC17791.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=129/SVJ, AND C57BL/6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PUMAG OR PUMA-G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Putative seven transmembrane spanning receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schaub A., Futterer A., Pfeffer K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9EP66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9EP66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGD; MGI:1933383; Pumag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "PUMA-G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     197
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   11
                                                                                                                          Local Similarity
les 178; Conserv
                                                             ω
                                   NG-SCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVAD
NGKNCCVFRDENIAKVLPPVLGLEFVFGLLGNGLALWIFCFHLKSWKSSRIFLFNLAVAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KQPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPSFPNFFSTLINRCLQR 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WTVPSSA---CD--PSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KMTGEPDNNRSTSVELTGDPNKT-RGAPEALMANSGEPWSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P34996; 1DDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           an interferon-gamma inducible gene in macrophages
                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                   46.9%; Score 868.5; DB 11; 55.6%; Pred. No. 1.8e-77; Mismatches 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                          ycoprotein; Receptor; Transmembrane
ccce52A2475777FC cRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence
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                                                                                                                                                                                DB 11; Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Euteleostomi;
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                                                                                                                          Gaps
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당 양

297 310

LRKKTLGEPDNNRSTSVELT 329

LKPKQPGHSKTQRPEEMPIS

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29 PAR 2017
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20 PAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Putat.
GPCR.
Homo sapiens (Human).
Homo sapiens (Homan).
Horia; Chordata;
Horia; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8TDS5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative G-protein coupled receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Identification of G protein-coupled genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases EMBL; AB083630; BAB89343.1; -.
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ
EMBL; AL121935; CAB99339.1; -
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                      01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
BA517H2.2 (G protein-coupled receptor 31).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                  GPR31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9NQ20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9NQ20
                                                                                                                  Almeida
                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 GSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FGMASMVAFWLSACRSLDLCTQLFHG----SLAFTYLNSVLDPVLYCFSSPNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --SARLYFLWTVPSSA---CDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSF 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQE-TAVSCESFIM----ESANGWHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LISNLPLRYDYYLLHETWRFGAAACKVNLFMLSTNRTASVVFLTAIALNRYLKVVQPHHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALYLLEFFLPLALILFAIVSIGLTIRNR-GLGGQAGPQRAMRVLAMVVAVYTICFLPSII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMFQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LSRASVGAAARVAGGLWVGI------LLLNGHLLLSTFSGPSCLSYRVGTKPSASLRWHQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kadowaki S., Haga T., Takaesu H., Mitaku
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               423 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 529; DB
Pred. No. 6.9e
48; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72ADA9F43A9EC051 CRC64;
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                                                                                     databases
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF140708; AAF26668.1; -.

MGD; MGI:98543; Tcp10c.
InterPro; IFR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.

PRINTS; PR00237; GPCRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "ORFless, intronless, and mutant transcription units complex responder (Tcr) locus."; Mamm. Genome 10:969-976(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE=99431663; PubMed=10501965;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G protein coupled receptor. TCP10C.
                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schimenti J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                      Receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CSAPSTVVATAVGVLLGLECGLGLLGNAVALWTFLFRVRVWKPYAVYLLNLALADLLLAA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMI
                                                                                                                                                           CRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMI 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VLMHIFQNLGSCRALCAVAHTSDVTGSLTYLHSVLNPVVYCFSSPTFRSSYRRV
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  SVPFFAAFYLKGKTWKLGHMPCQLLLFLLAFSCGVGVAFLMTVALDRYLHVVHPRLRVNL
                                                CLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNT 126
                                                                                                           CSAASTYVETAYGTMLTLECYLGLMGNAVALWTFFYRLKVWKPYAVYLFNLVVADLLLAT
                                                                                                                                                                                                                    104;
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PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          319 AA;
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                                                                                                                                                                                                                                                                                                                             35551 MW;
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                                                                                                                                                                                                                                           24.1%; Score 446.5; DB 11; 32.5%; Pred. No. 7.1e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 450.5; DB 4
Pred. No. 2.8e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2ACD0350AD7FB53A CRC64;
                                                                                                                                                                                                                                                                                                                                571F6DFB485BD7C4 CRC64;
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                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence update)
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Type five-like somatostatin receptor.
    Eukaryota;
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Best Local
                                                     InterPro; IPR000276; GPCR_Rhodpsn.
pfam; PF00001; 7tm_1; 1.
prIntrs; PR00237; GPCRRHODDPSN.
prOSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1
prOSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                 Dranoff J.A., O'Neill A.F., Franco A.M., Cai S.Y., Ballatori N., Boyer J.L., Nathanson M.H.; "A primitive ATP receptor from the little skate Ra. J. Biol. Chem. 275:30701-30706(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Raja erinacea (Little skate).
Eukaryota; Metazoa; Chordata; Craniata;
Elasmobranchii, Squalea; Hypnosqualea; I
Rajiformes; Rajidae; Raja.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2001 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
     SEQUENCE
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                                                                                                                                                                                                     HSSP; P34996; 1DDD.
                                                                                                                                                                                                                                EMBL; AF242850; AAG42684.1;
                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20459151; PubMed=10900200;
                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=7782;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P2Y receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Cloning and expression of a type five-like somatostatin goldfish.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Lin X., Peter R.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Carassius.
Cyprinidae; Carassius.
NCBI_TaxID=7957;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   205 YTAMLGFFFPLMVICLCYLLIVIKVKSASARAGLSKRGRSEKKVTRMVVIIVVVFVLCWL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHD--IM 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---KICSLKPKQPGHSKTQRPEE 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PFFIINILNLISTLPENSL---MTGIYFLTYILTYVNSCANPLLYSFLSDNFKRSFQQVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-SVSARLYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SARWRRPRVAKVINSMVWALSCLLTLPVII--YCDVQPELNTCNLSWPEPRDVWSTAFIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NGSSMAEEDST--KILAVIYLVVFVVGLTGNSLAIFVVLRYTKMKTATNMYILNLAVADE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADF
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357 AA;
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  41239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44136 MW;
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16,
  MW.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
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Pred. No. 2.
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  14604EE15DCBDB41 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EC12119A4B6CF9A8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Vertebrata; Chondrichthyes;
Pristiorajea; Batoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA
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                                                                                                                                                                                                                                                                                     Raja erinacea.";
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RESULT 10
Q90X57
ID Q90X57
ID Q90X5
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Best Local S
Matches 87
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cheng A.W., Tsim K.W.;
"Cloning of xenopus P2Y1 Receptor.";
"Submitted (QCT-2001) to the EMBL/GenBank/DDBJ databases
EMBL; AF432354; AAL27614.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xenopus laevis (African clawed frog),
Eukaryota; Metazoa; Chordata; Craniata; Ver
Amphibia; Batrachia; Anura; Mesobatrachia;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q90X57;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00001; 7tm_1; PROSITE; PS00237; G_PI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P2Y1 nucleotide receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00237; G_PROTEIN_RECEP_F1_1;
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000276; GPCR_Rhodpsn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VCVWITVMAGISPILYFSRTGLRRNKTNTCYDTTSKELLETYFIYSMSTTF-----FGFC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LPIMYIIVFVTGFIGNSVALWMFIFHMRPWSSITIYMFNLVLADLFYVFSLPILIFYYFN 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KPKQPGHSKTQRPEEMPISNLGRRSCISV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPFATILVCYGFIVKALISNDM--KTPLRGKSVRLVIIVLAVFAISYLPFHVMKNLNLQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLP-----SVSA 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KTDWIFGELLCKLXRFIFHVNLYGSILFLTCISVHRYTGVVHPMKSLGRLKKK-SATIVC
                       PLGITLFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLP--
                                                                                   LVWFIVIAGISPILFFSGTGIRKNKTITCFDTSSDEYLRSYFIYSM-----CTTVFGFCI
                                                                                                                                                                                                                                                                                                                                                 MPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMICLPFRTDYYLR
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                                                                                                                                         TLWALVILGTVYLLLENHLCVQET-AVSC-----ESFIMESANGWHDIMFQLEFFM 187
                                                                                                                                                                                               KTDWIFGDALCKLQRFLFHVNLYGSILFLTCISVHRYTGVVHPLKSLGRLKKKNSIYISA 161
                                                                                                                                                                                                                                                       RRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVAAGIVC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41002 MW;
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26.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         18.4%; Score 341; DB 13; 29.0%; Pred. No. 2.1e-25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 361;
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                             -SVSAR
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RESULT 12
Q9H1C0
ID Q9H1C
AC Q9H1C
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Best Local Similarity
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Q9H1C0;
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01-MAR-2001 (TIEMBLIEL 16, Last
01-MAR-2002 (TIEMBLIEL 20, Last
01-MAR-2002 (TIEMBLIEL 30, Last
Somatostatin receptor type two.
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PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

G-protein coupled receptor; Glycoprotein; Receptor; Tr G-protein coupled receptor; Glycoprotein; CRC64; SEQUENCE 380 AA; 43146 MW; CE897FF7537CFA30 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lin X., Janovick J.A., Cardenas R., Conn P.M., Peter R.E.;
"Molecular cloning and expression of a type-two somatostatin receptor in goldfish brain and pituitary.";
Mol. Cell. Endocrinol. 166:75-87(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=7957;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Carassius auratus (Goldfish).
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Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED EMBL; AF139597; AAF98367.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20453044; PubMed=10996426;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LDF---QSPEMCNENDRVYATYQVTRGLASLNSCVDPTLYFLAGDTFRR---
                                                                                                                                                                                                                                                                                                                    AIQLSLLHWPFGSAICRVYLTADSMNQFTSIFFLTVMSFDRYLAVVHPIKSTKWRKPRMA 167
                                                                                                                                                                                                                                                                                                                                                                                                                        TISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMICLPFRT 72
                                                                                                       VTG-----TVPTT---PVLKSTFDEVVVLGYANSCANPILYAFLSDNFKKSFQNVL
                                                                                                                                        VSARLYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPK-FYNKL
                                                                                                                                                                                                            PLGIILFCSFKIVWSLR----RRQQLARQARMKKATRFIMVVAIVFITCYLP-----S 236
                                                                                                                                                                                                                                              KSISLAMWVISLLVNLPIMIYSGVNVKKNEARTCIMLWPEPQNTYYTVFIFYTFFMGFFL 227
                                                                                                                                                                                                                                                                                 AGIVCTLWALVILGTVYLLLENHLCVQET-AVSCESFIMESANGWHDIM----FQLEFFM 187
                                                                                                                                                                                                                                                                                                                                                    DYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVA 132
                                                                                                                                                                                                                                                                                                                                                                                         TSSVVITFVYFVVCAVGLCGNALVMYVILRYAKMKTVTNIYILNLAVADVLCMLSLPF-I 107
                                                                                                                                                                         PLIVICMCYLLIVIKVKSSGMRVCSSKRKRSERKVTRMVSIVVVVFVLCWLPFYVFNVTS
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                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17.8%;
31.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 329.5; DB Pred. No. 3e-24; 2; Mismatches 1
                     PRT;
                     372
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Best Local
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White K.E., Evans W.E., O'Riordan J.L.H., Speer M.C.,
Lorenz-Depiereux B., Grabowski M., Meitinger T., Strou
"Autosomal dominant hypophosphataemic rickets is asso-
"nutations in FGF23.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lewis T., Evans J.F., George S.R., O'Dowd B.F.; The state of the state
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=21458557; PubMed=11574155;
Lee D.K., Nguyen T., Lynch K.R., Cheng R., Vanti W.B.,
Lewis T., Evans J.F., George S.R., O'Dowd B.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative G protein-coupled receptor 92 (Putative G-protein coupled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genome sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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295
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                                                                                                                                                                                                                                                                                                                                                                120
                                                                                                                                                                                                                                                                                                                                                                                                                 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 TISQVMP-----PLLIVAFVLGALG---NGVALCGFCFHMKTWKPSTVYLFNLAV
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                                             LVYYFSSPSF 285
                                                                                                                                      FIMVVAIVFITCYLP-----SVSARLYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDP
LVYYFSAEGF
                                                                                                                                                                                                                                             FIMESANGWHDIMF-----QLEFFMPLGIILFCSFKIVWSLRRQQLARQARMKKATR
                                                                                        LLLANLVIFLLCFVPYNSTLAVYGLLRSKLVAASVPARDRVRGVLMVMVLLAGANCVLDP
                                                                                                                                                                                            F---SDELWKGRLLPLVLLAEALGFLLPLAAVVYSSGRVFWTLARPDATQSQ-RRRKTVR
                                                                                                                                                                                                                                                                                                   PLRLRHLRRPRVARLLCLGVWALILVFAVPAARVHRPSRCRYRDLEVRLCF-----
                                                                                                                                                                                                                                                                                                                                                                                                 SDLLFTLSLPVRLSYY-ALHHWPFPDLLCQTTGAIFQMNMYGSCIFLMLINVDRYAAIVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TNSSVLPCPDYRPTHRLHLVVYSLVLAA-GLPLNALALWVFLRALRVHSVVSVYMCNLAA 66
                                                                                                                                                                                                                                                                                                                                                        PHHAVNTISTRVAAGIVCTLWALVILGTV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pro; IPR000276; GPCR_Rhodpsn.
PF00001; 7tm_1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tted (APR-2002) to the EMBL/GenBank/DDBJ databases AJ272207; CAC03715.1; -. AP411112; AAL26483.1; -. AB083600; BAB89313.1; -. AB083600; BAB89313.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P34996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       372 AA; 41346 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kadowaki S., Haga T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26:345-348(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 305;
Pred. No. 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BA35709084BB6D84 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Takaesu H., Mitaku
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .8e-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                125;
                                                                                                                                                                                                                                                                                                                                                   --YLLLENHLCVQETAVSCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                M.C., Econs M.J.,
Strom T.M.;
associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S.;
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Eutheria; Primates;

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RESULT
Q96GE0
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ACCOMMENS
OX OX OX OX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                            01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation updat
                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                       Unknown (Protein for IMAGE: 3354783) (Fragment).
                                                                                                                                                                                                                                    Q96GE0;
                                                                                                                                                                                                                                                            Q96GE0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00237; GPCRRHODOPSN.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.

G-protein coupled receptor; Glycoprotein; Receptor; Trigerous Coupled Receptor; C07010EDB81110EB CRC64;
                                                                               Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; P34996; 1DDD.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY) -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS. EMBL; AF254119; AAF66063.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia; Eutheria; Cetartiodactyla;
Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence up
01-MAR-2002 (TrEMBLrel. 20, Last annotation
Angiotensin II type 1 receptor.
                                                                                                                                                                                                                                                                                                                                                                                                               328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ovis aries (Sheep).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Endocr. Res. 0:0-0(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R) cDNA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bird I.M., Millican D.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=ADRENAL CORTEX;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9N0U1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9N0U1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  149 CIIIWLLAGLASLPTIIHRNVFFIENTNITVCAFHYESQNSTLPVGLGLTKNILGFLFPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Isolation of a Full Length Ovine Angiotensin II Type-1 Receptor (AT1-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 VMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMICLPFRTDYYL 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIV--FITCYLP----SVSARLYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C-TLWALVILGTVYLLL-ENHLCVQETAVSCESFIMESANGWHDIMFQLE----FFMPL 189
                                                                                                                                                                                                                                                                                                                                                                                                            SNLSTKMSTLSYRPSENGNSSTKKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----NKLKICSLKPKQPGHSKTQRP 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LGLIRDCKIEDIVDTAMPITICLAYFNNCLNPLFYGFLGKKFKKYFLQLLKYIPPKAKSH 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -LIILTSYTLIWKTLKKAYEIQKNKPRKDDIFKIILAIVLFFFFSWVPHQIFTFMDVLIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEYRWPFGNYLCKIASGSVSFNLYASVFLLTCLSIDRYLAIVHPMKS-RLRRTMLVAKVT 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVAAGIV 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
               Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16.4%; Score 303.5;
24.9%; Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68;
                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                            352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                            346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           update)
                                                                                                                                   update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             143;
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8

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RESULT 15
Q96TF2
ID Q96TF
AC Q96TF
DT 01-DE
DT 01-MA
DE SOMAT
GN SSTR2
OS HOMO
OC EUKAR
OC Mamma
OX NCBI_
RN [1]
RP SEQUE
RX MEDL;
RA Peter
RT Senat
RI HO1.
DR EMBL;
DR Intex
DR PROSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Qy
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Best Local S
Matches 90
                              Query Match
Best Local Similarity
               Matches
                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=20084417; PubMed=10619399;
Petersenn S., Rasch A.C., Presch S., Beil F.U., Sc.
"Genomic structure and transcriptional regulation
"Genomic structure and transcriptional regulation
                                                                                                                 InterPro; IPR000276; GPCR_Rhodpsn.

Pfam; PF00001; 7tm_1; 1.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.

PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.

SEQUENCE 356 AA; 40006 MW; D10FA237FAED61F3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                       somatostatin receptor type 2.";
Mol. Cell. Endocrinol. 157:75-85(1999).
EMBL; AF184174; AAF42810.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Somatostatin receptor 2B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q96TF2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606
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InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=EYE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              307 VK 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               297 LK 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 LYFLWTVPSSAC----DPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        194 FLVPLTIICLCYLFIIIKVKSSGIRVGSSKRKKSEKKVTRMVSIVVAVFIFCWLP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78
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nes 90; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -FYIFNVSSVSMAISPTPALKGMFDFVVVLTYANSCANPILYAFLSDNFKKSFQNV-LCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FFMPLGIILFCSFKIVWSLR----RRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KMITMAVWGVSLLVILPIMIYAGLRSN---QWGRSSCTINWPGESGAWYTGFIIYTFILG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGIVCTLWA----LVILG-TVYLLLENHLCVQETAVSCESFIMESANGWHD----IMFQLE 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -MQVALVHWPFGKAICRVVMTVDGINQFTSIFCLTVMSIDRYLAVVHPIKSAKWRRPRTA 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DYYLRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TSNAVLTFIYFVVCIIGLCGNTLVIYVILRYAKMKTITNIYILNLAIADELFMLGLPFLA 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMICLPFRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     346 AA; 38790 MW; EA073A6CC05FEB72 CRC64;
            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
   16.3%; Score 302.5; DB 4; 29.8%; Pred. No. 1.3e-21; cive 50; Mismatches 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 302.5; DB 4; Length
; Pred. No. 1.3e-21;
50; Mismatches 135; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       356
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                                                          DB 4; Length 356;
                                                                                                                                                                                                                                                                                                                                                    Schulte H.M.; on of the human
      Indels
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   27;
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Gaps
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   9;
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330 VK 331
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                                  297 LK 298
                                                                                              241 LYFLWTVPSSAC----DPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICS
                                                                                                                                                                                                                                                                                  101 -MQVALVHWPFGKAICRVVMTVDGINQFTSIFCLTVMSIDRYLAVVHPIKSAKWRRPRTA
                                                                                                                                                                                                                                                                                                                                                                             13 TISQVMPPLLIVAFVLGALGGGGGGHMKTWKPSTVYLFNLAVADFLLMICLPFRT 72
                                                                                                                                                                                                                                                                                                                                                         41 TSNAVLTFIYFVVCIIGLCGNTLVIYVILRYAKMKTITNIYILNLAIADELFMLGLPFLA
                                                                                                                                                             FFMPLGIILFCSFKIVWSLR----RRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR
                                                                                                                                                                                                          KMITMAVWGVSLLVILPIMIYAGLRSN---QWGRSSCTINWPGESGAWYTGFIIYTFILG
                                                                                                                                                                                                                                                AGIVCTLWA----LVILG-TVYLLLENHLCVQETAVSCESFIMESANGWHD----IMFQLE 184
                                                                -FYIENVSSVSMAISPTPALKGMFDFVVVLTYANSCANPILYAFLSDNFKKSFQNV-LCL
                                                                                                                                      FLVPLTIICLCYLFIIIKVKSSGIRVGSSKRKKSEKKVTRMVSIVVAVFIFCWLP----
                                                                                                                                                                                                                                                                                                               DYYLRRHWAFGDIPCRVGLETLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVA 132
                                                                                                                                                                          240
                                                                                                                                                                                                              216
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Search completed: March 26, 2003, 19:38:47 Job time: 37 secs

